

SEQUENCE LISTING  
AP20 Rec'd 10 MAY 2006

<110> James, David  
Cooney, Gregory J  
Molero-Navajas, Juan C

<120> Methods of validating target for modulating insulin action,  
screening for modulators of insulin action and therapeutic uses  
thereof

<130> 42-000500US

<150> AU 2003906286  
<151> 2003-11-14

<150> PCT/AU2004/001572  
<151> 2004-11-15

<150> AU 2003906285  
<151> 2003-11-14

<160> 268

<170> PatentIn version 3.3

<210> 1  
<211> 153  
<212> PRT  
<213> Mus musculus

<400> 1

Met Ala Gly Asn Val Lys Lys Ser Ser Gly Ala Gly Gly Gly Ser  
1 5 10 15

Gly Gly Ser Gly Ala Gly Gly Leu Ile Gly Leu Met Lys Asp Ala Phe  
20 25 30

Gln Pro His His His His His Leu Ser Pro His Pro Pro Cys Thr  
35 40 45

Val Asp Lys Lys Met Val Glu Lys Cys Trp Lys Leu Met Asp Lys Val  
50 55 60

Val Arg Leu Cys Gln Asn Pro Asn Val Ala Leu Lys Asn Ser Pro Pro  
65 70 75 80

Tyr Ile Leu Asp Leu Leu Pro Asp Thr Tyr Gln His Leu Arg Thr Val  
85 90 95

Leu Ser Arg Tyr Glu Gly Lys Met Glu Thr Leu Gly Glu Asn Glu Tyr

100

105

110

Phe Arg Val Phe Met Glu Asn Leu Met Lys Lys Thr Lys Gln Thr Ile  
115 120 125

Ser Leu Phe Lys Glu Gly Lys Glu Arg Met Tyr Glu Glu Asn Ser Gln  
130 135 140

Pro Arg Arg Asn Leu Thr Lys Leu Ser  
145 150

<210> 2  
<211> 896  
<212> PRT  
<213> Mus musculus

<400> 2

Met Ala Gly Asn Val Lys Lys Ser Ser Gly Ala Gly Gly Gly Ser  
1 5 10 15

Gly Gly Ser Gly Ala Gly Gly Leu Ile Gly Leu Met Lys Asp Ala Phe  
20 25 30

Gln Pro His His His His His His Leu Ser Pro His Pro Pro Cys Thr  
35 40 45

Val Asp Lys Lys Met Val Glu Lys Cys Trp Lys Leu Met Asp Lys Val  
50 55 60

Val Arg Leu Cys Gln Asn Pro Asn Val Ala Leu Lys Asn Ser Pro Pro  
65 70 75 80

Tyr Ile Leu Asp Leu Leu Pro Asp Thr Tyr Gln His Leu Arg Thr Val  
85 90 95

Leu Ser Arg Tyr Glu Gly Lys Met Glu Thr Leu Gly Glu Asn Glu Tyr  
100 105 110

Phe Arg Val Phe Met Glu Asn Leu Met Lys Lys Thr Lys Gln Thr Ile  
115 120 125

Ser Leu Phe Lys Glu Gly Lys Glu Arg Met Tyr Glu Glu Asn Ser Gln  
130 135 140

Pro Arg Arg Asn Leu Thr Lys Leu Ser Leu Ile Phe Ser His Met Leu  
145 150 155 160

Ala Glu Leu Lys Gly Ile Phe Pro Ser Gly Leu Phe Gln Gly Asp Thr  
165 170 175

Phe Arg Ile Thr Lys Ala Asp Ala Ala Glu Phe Trp Arg Lys Ala Phe  
180 185 190

Gly Glu Lys Thr Ile Val Pro Trp Lys Ser Phe Arg Gln Ala Leu His  
195 200 205

Glu Val His Pro Ile Ser Ser Gly Leu Glu Ala Met Ala Leu Lys Ser  
210 215 220

Thr Ile Asp Leu Thr Cys Asn Asp Tyr Ile Ser Val Phe Glu Phe Asp  
225 230 235 240

Ile Phe Thr Arg Leu Phe Gln Pro Trp Ser Ser Leu Leu Arg Asn Trp  
245 250 255

Asn Ser Leu Ala Val Thr His Pro Gly Tyr Met Ala Phe Leu Thr Tyr  
260 265 270

Asp Glu Val Lys Ala Arg Leu Gln Lys Phe Ile His Lys Pro Gly Ser  
275 280 285

Tyr Ile Phe Arg Leu Ser Cys Thr Arg Leu Gly Gln Trp Ala Ile Gly  
290 295 300

Tyr Val Thr Ala Asp Gly Asn Ile Leu Gln Thr Ile Pro His Asn Lys  
305 310 315 320

Pro Leu Phe Gln Ala Leu Ile Asp Gly Phe Arg Glu Gly Phe Tyr Leu  
325 330 335

Phe Pro Asp Gly Arg Asn Gln Asn Pro Asp Leu Thr Gly Leu Cys Glu  
340 345 350

Pro Thr Pro Gln Asp His Ile Lys Val Thr Gln Ile Cys Ala Glu Asn  
355 360 365

Asp Lys Asp Val Lys Ile Glu Pro Cys Gly His Leu Met Cys Thr Ser  
370 375 380

Cys Leu Thr Ser Trp Gln Glu Ser Glu Gly Gln Gly Cys Pro Phe Cys  
385 390 395 400

Arg Cys Glu Ile Lys Gly Thr Glu Pro Ile Val Val Asp Pro Phe Asp  
405 410 415

Pro Arg Gly Ser Gly Ser Leu Leu Arg Gln Gly Ala Glu Gly Ala Pro  
420 425 430

Ser Pro Asn Tyr Asp Asp Asp Asp Glu Arg Ala Asp Asp Ser Leu  
435 440 445

Phe Met Met Lys Glu Leu Ala Gly Ala Lys Val Glu Arg Pro Ser Ser  
450 455 460

Pro Phe Ser Met Ala Pro Gln Ala Ser Leu Pro Pro Val Pro Pro Arg  
465 470 475 480

Leu Asp Leu Leu Gln Gln Arg Ala Pro Val Pro Ala Ser Thr Ser Val  
485 490 495

Leu Gly Thr Ala Ser Lys Ala Ala Ser Gly Ser Leu His Lys Asp Lys  
500 505 510

Pro Leu Pro Ile Pro Pro Thr Leu Arg Asp Leu Pro Pro Pro Pro Pro  
515 520 525

Pro Asp Arg Pro Tyr Ser Val Gly Ala Glu Thr Arg Pro Gln Arg Arg  
530 535 540

Pro Leu Pro Cys Thr Pro Gly Asp Cys Pro Ser Arg Asp Lys Leu Pro  
545 550 555 560

Pro Val Pro Ser Ser Arg Pro Gly Asp Ser Trp Leu Ser Arg Thr Ile  
565 570 575

Pro Lys Val Pro Val Ala Thr Pro Asn Pro Gly Asp Pro Trp Asn Gly  
580 585 590

Arg Glu Leu Thr Asn Arg His Ser Leu Pro Phe Ser Leu Pro Ser Gln

595

600

605

Met Glu Pro Arg Ala Asp Val Pro Arg Leu Gly Ser Thr Phe Ser Leu  
610 615 620

Asp Thr Ser Met Thr Met Asn Ser Ser Pro Val Ala Gly Pro Glu Ser  
625 630 635 640

Glu His Pro Lys Ile Lys Pro Ser Ser Ser Ala Asn Ala Ile Tyr Ser  
645 650 655

Leu Ala Ala Arg Pro Leu Pro Met Pro Lys Leu Pro Pro Gly Glu Gln  
660 665 670

Gly Glu Ser Glu Glu Asp Thr Glu Tyr Met Thr Pro Thr Ser Arg Pro  
675 680 685

Val Gly Val Gln Lys Pro Glu Pro Lys Arg Pro Leu Glu Ala Thr Gln  
690 695 700

Ser Ser Arg Ala Cys Asp Cys Asp Gln Gln Ile Asp Ser Cys Thr Tyr  
705 710 715 720

Glu Ala Met Tyr Thr Ile Gln Ser Gln Ala Leu Ser Val Ala Glu Asn  
725 730 735

Ser Ala Ser Gly Glu Gly Asn Leu Ala Thr Ala His Thr Ser Thr Gly  
740 745 750

Pro Glu Glu Ser Glu Asn Glu Asp Asp Gly Tyr Asp Val Pro Lys Pro  
755 760 765

Pro Val Pro Ala Val Leu Ala Arg Arg Thr Leu Ser Asp Ile Ser Asn  
770 775 780

Ala Ser Ser Ser Phe Gly Trp Leu Ser Leu Asp Gly Asp Pro Thr Asn  
785 790 795 800

Phe Asn Glu Gly Ser Gln Val Pro Glu Arg Pro Pro Lys Pro Phe Pro  
805 810 815

Arg Arg Ile Asn Ser Glu Arg Lys Ala Ser Ser Tyr Gln Gln Gly Gly  
820 825 830

Gly Ala Thr Ala Asn Pro Val Ala Thr Ala Pro Ser Pro Gln Leu Ser  
835 840 845

Ser Glu Ile Glu Arg Leu Met Ser Gln Gly Tyr Ser Tyr Gln Asp Ile  
850 855 860

Gln Lys Ala Leu Val Ile Ala His Asn Asn Ile Glu Met Ala Lys Asn  
865 870 875 880

Ile Leu Arg Glu Phe Val Ser Ile Ser Ser Pro Ala His Val Ala Thr  
885 890 895

<210> 3  
<211> 906  
<212> PRT  
<213> Homo sapiens

<400> 3

Met Ala Gly Asn Val Lys Lys Ser Ser Gly Ala Gly Gly Thr Gly  
1 5 10 15

Ser Gly Gly Ser Gly Ser Gly Leu Ile Gly Leu Met Lys Asp Ala  
20 25 30

Phe Gln Pro His His His His His His His Leu Ser Pro His Pro Pro  
35 40 45

Gly Thr Val Asp Lys Lys Met Val Glu Lys Cys Trp Lys Leu Met Asp  
50 55 60

Lys Val Val Arg Leu Cys Gln Asn Pro Lys Leu Ala Leu Lys Asn Ser  
65 70 75 80

Pro Pro Tyr Ile Leu Asp Leu Leu Pro Asp Thr Tyr Gln His Leu Arg  
85 90 95

Thr Ile Leu Ser Arg Tyr Glu Gly Lys Met Glu Thr Leu Gly Glu Asn  
100 105 110

Glu Tyr Phe Arg Val Phe Met Glu Asn Leu Met Lys Lys Thr Lys Gln  
115 120 125

Thr Ile Ser Leu Phe Lys Glu Gly Lys Glu Arg Met Tyr Glu Glu Asn  
130 135 140

Ser Gln Pro Arg Arg Asn Leu Thr Lys Leu Ser Leu Ile Phe Ser His  
145 150 155 160

Met Leu Ala Glu Leu Lys Gly Ile Phe Pro Ser Gly Leu Phe Gln Gly  
165 170 175

Asp Thr Phe Arg Ile Thr Lys Ala Asp Ala Ala Glu Phe Trp Arg Lys  
180 185 190

Ala Phe Gly Glu Lys Thr Ile Val Pro Trp Lys Ser Phe Arg Gln Ala  
195 200 205

Leu His Glu Val His Pro Ile Ser Ser Gly Leu Glu Ala Met Ala Leu  
210 215 220

Lys Ser Thr Ile Asp Leu Thr Cys Asn Asp Tyr Ile Ser Val Phe Glu  
225 230 235 240

Phe Asp Ile Phe Thr Arg Leu Phe Gln Pro Trp Ser Ser Leu Leu Arg  
245 250 255

Asn Trp Asn Ser Leu Ala Val Thr His Pro Gly Tyr Met Ala Phe Leu  
260 265 270

Thr Tyr Asp Glu Val Lys Ala Arg Leu Gln Lys Phe Ile His Lys Pro  
275 280 285

Gly Ser Tyr Ile Phe Arg Leu Ser Cys Thr Arg Leu Gly Gln Trp Ala  
290 295 300

Ile Gly Tyr Val Thr Ala Asp Gly Asn Ile Leu Gln Thr Ile Pro His  
305 310 315 320

Asn Lys Pro Leu Phe Gln Ala Leu Ile Asp Gly Phe Arg Glu Gly Phe  
325 330 335

Tyr Leu Phe Pro Asp Gly Arg Asn Gln Asn Pro Asp Leu Thr Gly Leu  
340 345 350

Cys Glu Pro Thr Pro Gln Asp His Ile Lys Val Thr Gln Glu Gln Tyr

355

360

365

Glu Leu Tyr Cys Glu Met Gly Ser Thr Phe Gln Leu Cys Lys Ile Cys  
370 375 380

Ala Glu Asn Asp Lys Asp Val Lys Ile Glu Pro Cys Gly His Leu Met  
385 390 395 400

Cys Thr Ser Cys Leu Thr Ser Trp Gln Glu Ser Glu Gly Gln Gly Cys  
405 410 415

Pro Phe Cys Arg Cys Glu Ile Lys Gly Thr Glu Pro Ile Val Val Asp  
420 425 430

Pro Phe Asp Pro Arg Gly Ser Gly Ser Leu Leu Arg Gln Gly Ala Glu  
435 440 445

Gly Ala Pro Ser Pro Asn Tyr Asp Asp Asp Asp Glu Arg Ala Asp  
450 455 460

Asp Thr Leu Phe Met Met Lys Glu Leu Ala Gly Ala Lys Val Glu Arg  
465 470 475 480

Pro Pro Ser Pro Phe Ser Met Ala Pro Gln Ala Ser Leu Pro Pro Val  
485 490 495

Pro Pro Arg Leu Asp Leu Leu Pro Gln Arg Val Cys Val Pro Ser Ser  
500 505 510

Ala Ser Ala Leu Gly Thr Ala Ser Lys Ala Ala Ser Gly Ser Leu His  
515 520 525

Lys Asp Lys Pro Leu Pro Val Pro Pro Thr Leu Arg Asp Leu Pro Pro  
530 535 540

Pro Pro Pro Pro Asp Arg Pro Tyr Ser Val Gly Ala Glu Ser Arg Pro  
545 550 555 560

Gln Arg Arg Pro Leu Pro Cys Thr Pro Gly Asp Cys Pro Ser Arg Asp  
565 570 575

Lys Leu Pro Pro Val Pro Ser Ser Arg Leu Gly Asp Ser Trp Leu Pro  
580 585 590

Arg Pro Ile Pro Lys Val Pro Val Ser Ala Pro Ser Ser Ser Asp Pro  
595 600 605

Trp Thr Gly Arg Glu Leu Thr Asn Arg His Ser Leu Pro Phe Ser Leu  
610 615 620

Pro Ser Gln Met Glu Pro Arg Pro Asp Val Pro Arg Leu Gly Ser Thr  
625 630 635 640

Phe Ser Leu Asp Thr Ser Met Ser Met Asn Ser Ser Pro Leu Val Gly  
645 650 655

Pro Glu Cys Asp His Pro Lys Ile Lys Pro Ser Ser Ser Ala Asn Ala  
660 665 670

Ile Tyr Ser Leu Ala Ala Arg Pro Leu Pro Val Pro Lys Leu Pro Pro  
675 680 685

Gly Glu Gln Cys Glu Gly Glu Asp Thr Glu Tyr Met Thr Pro Ser  
690 695 700

Ser Arg Pro Leu Arg Pro Leu Asp Thr Ser Gln Ser Ser Arg Ala Cys  
705 710 715 720

Asp Cys Asp Gln Gln Ile Asp Ser Cys Thr Tyr Glu Ala Met Tyr Asn  
725 730 735

Ile Gln Ser Gln Ala Pro Ser Ile Thr Glu Ser Ser Thr Phe Gly Glu  
740 745 750

Gly Asn Leu Ala Ala Ala His Ala Asn Thr Gly Pro Glu Glu Ser Glu  
755 760 765

Asn Glu Asp Asp Gly Tyr Asp Val Pro Lys Pro Pro Val Pro Ala Val  
770 775 780

Leu Ala Arg Arg Thr Leu Ser Asp Ile Ser Asn Ala Ser Ser Ser Phe  
785 790 795 800

Gly Trp Leu Ser Leu Asp Gly Asp Pro Thr Thr Asn Val Thr Glu Gly  
805 810 815

Ser Gln Val Pro Glu Arg Pro Pro Lys Pro Phe Pro Arg Arg Ile Asn  
820 825 830

Ser Glu Arg Lys Ala Gly Ser Cys Gln Gln Gly Ser Gly Pro Ala Ala  
835 840 845

Ser Ala Ala Thr Ala Ser Pro Gln Leu Ser Ser Glu Ile Glu Asn Leu  
850 855 860

Met Ser Gln Gly Tyr Ser Tyr Gln Asp Ile Gln Lys Ala Leu Val Ile  
865 870 875 880

Ala Gln Asn Asn Ile Glu Met Ala Lys Asn Ile Leu Arg Glu Phe Val  
885 890 895

Ser Ile Ser Ser Pro Ala His Val Ala Thr  
900 905

<210> 4  
<211> 2483  
<212> PRT  
<213> homo sapiens

<400> 4

Met Val Leu Leu Leu Cys Leu Ser Cys Leu Ile Phe Ser Cys Leu Thr  
1 5 10 15

Phe Ser Trp Leu Lys Ile Trp Glu Lys Met Thr Asp Ser Lys Pro Ile  
20 25 30

Thr Lys Ser Lys Ser Glu Ala Asn Leu Ile Pro Ser Gln Glu Pro Phe  
35 40 45

Pro Ala Ser Asp Asn Ser Gly Glu Thr Pro Gln Arg Asn Gly Glu Gly  
50 55 60

His Thr Leu His Lys Asp Thr Gln Pro Gly Arg Ala Gln Pro Pro Thr  
65 70 75 80

Lys Ala Gln Arg Ser Gly Arg Arg Asn Ser Leu Pro Pro Ser Arg  
85 90 95

Gln Lys Pro Pro Arg Asn Pro Leu Ser Ser Asp Ala Ala Pro Ser

100

105

110

Pro Glu Leu Gln Ala Asn Gly Thr Gly Thr Gln Gly Leu Glu Ala Thr  
115 120 125

Asp Thr Asn Gly Leu Ser Ser Ser Ala Arg Pro Gln Gly Ser Lys Leu  
130 135 140

Val Pro Ser Lys Glu Asp Lys Lys Gln Ala Asn Ile Lys Arg Gln Leu  
145 150 155 160

Met Thr Asn Phe Ile Leu Gly Ser Phe Asp Asp Tyr Ser Ser Asp Glu  
165 170 175

Asp Ser Val Ala Gly Ser Ser Arg Glu Ser Thr Arg Lys Gly Ser Arg  
180 185 190

Ala Ser Leu Gly Ala Leu Ser Leu Glu Ala Tyr Leu Thr Thr Gly Glu  
195 200 205

Ala Glu Thr Arg Val Pro Thr Met Arg Pro Ser Met Ser Gly Leu His  
210 215 220

Leu Val Lys Arg Gly Arg Glu His Lys Lys Leu Asp Leu His Arg Asp  
225 230 235 240

Phe Thr Val Ala Ser Pro Ala Glu Phe Val Thr Arg Phe Gly Gly Asp  
245 250 255

Arg Val Ile Glu Lys Val Leu Ile Ala Asn Asn Gly Ile Ala Ala Val  
260 265 270

Lys Cys Met Arg Ser Ile Arg Arg Trp Ala Tyr Glu Met Phe Arg Asn  
275 280 285

Glu Arg Ala Ile Arg Phe Val Arg Met Val Thr Pro Glu Asp Leu Lys  
290 295 300

Ala Asn Ala Glu Tyr Ile Lys Met Ala Asp His Tyr Gly Pro Ala Pro  
305 310 315 320

Gly Gly Pro Asn Asn Asn Asn Tyr Ala Asn Val Glu Leu Ile Val Asp  
325 330 335

Ile Ala Lys Arg Ile Pro Leu Gln Ala Val Trp Ala Gly Trp Gly His  
340 345 350

Ala Leu Glu Asn Pro Lys Leu Pro Glu Leu Leu Cys Lys Asn Gly Val  
355 360 365

Ala Phe Leu Gly Pro Pro Arg Leu Arg Pro Met Val Gly Leu Gly Asp  
370 375 380

Lys Ile Ala Ser Thr Val Val Ala Gln Thr Leu Gln Val Pro Thr Leu  
385 390 395 400

Pro Arg Ser Gly Ser Ala Leu Thr Val Glu Trp Thr Glu Asp Asp Leu  
405 410 415

Gln Gln Gly Lys Arg Ile Ser Val Pro Glu Asp Val Tyr Asp Lys Gly  
420 425 430

Cys Val Lys Asp Val Asp Glu Gly Leu Glu Ala Ala Glu Arg Ile Gly  
435 440 445

Phe Pro Leu Met Ile Lys Ala Ser Glu Gly Gly Gly Lys Gly Ile  
450 455 460

Arg Glu Thr Glu Ser Ala Glu Asp Phe Pro Ile Leu Phe Arg Gln Val  
465 470 475 480

Gln Ser Glu Ile Pro Gly Ser Pro Ile Phe Leu Met Lys Leu Ala Gln  
485 490 495

His Ala Arg His Leu Glu Val Gln Ile Leu Ala Asp Gln Tyr Asn  
500 505 510

Ala Val Ser Leu Phe Gly Arg Asp Cys Ser Ile Gln Arg Arg His Gln  
515 520 525

Lys Ile Val Glu Glu Ala Pro Ala Thr Ile Ala Pro Leu Ala Ile Phe  
530 535 540

Glu Phe Met Glu Gln Cys Ala Ile Arg Leu Ala Lys Thr Val Gly Tyr  
545 550 555 560

Val Ser Ala Gly Thr Val Glu Tyr Leu Tyr Ser Gln Asp Gly Ser Phe  
565 570 575

His Phe Leu Glu Leu Asn Pro Arg Leu Gln Val Glu His Pro Cys Thr  
580 585 590

Glu Met Ile Ala Asp Val Asn Leu Pro Ala Ala Gln Leu Gln Ile Ala  
595 600 605

Met Gly Ala Pro Leu His Arg Leu Lys Asp Ile Arg Leu Leu Tyr Gly  
610 615 620

Glu Ser Pro Trp Gly Asp Ser Pro Ile Ser Phe Glu Asn Ser Ala His  
625 630 635 640

Leu Pro Cys Pro Arg Gly His Val Ile Ala Thr Arg Ile Thr Ser Glu  
645 650 655

Asn Pro Asp Glu Gly Phe Lys Pro Ser Ser Gly Thr Val Gln Glu Leu  
660 665 670

Asn Phe Arg Ser Ser Lys Asn Val Trp Gly Tyr Phe Thr Val Ala Ala  
675 680 685

Thr Gly Gly Leu His Glu Phe Ala Ile Ser Gln Phe Gly His Cys Phe  
690 695 700

Ser Trp Gly Glu Asn Arg Lys Glu Ala Ile Ser Asn Met Val Val Ala  
705 710 715 720

Leu Lys Glu Leu Ser Leu Arg Gly Asp Phe Arg Thr Thr Val Glu Tyr  
725 730 735

Leu Ile Asn Leu Leu Glu Thr Glu Ser Phe Gln Asn Asn Tyr Ile Asp  
740 745 750

Thr Gly Trp Leu Asp Tyr Leu Ile Ala Glu Lys Val Gln Lys Lys Pro  
755 760 765

Asn Ile Met Leu Gly Val Val Cys Gly Ala Leu Glu Arg Gly Asp Ala  
770 775 780

Met Phe Arg Thr Cys Met Thr Asp Phe Leu His Ser Leu Glu Arg Gly  
785 790 795 800

Gln Val Leu Pro Ala Asp Ser Leu Leu Asn Leu Val Asp Val Glu Leu  
805 810 815

Ile Tyr Glu Gly Val Lys Tyr Ile Leu Lys Val Thr Arg Gln Ser Leu  
820 825 830

Thr Met Phe Val Leu Ile Met Asn Gly Cys His Ile Glu Ile Asp Ala  
835 840 845

His Arg Leu Asn Asp Gly Gly Leu Leu Leu Ser Tyr Asn Gly Asn Ser  
850 855 860

Tyr Thr Thr Tyr Met Lys Glu Glu Val Asp Ser Tyr Arg Thr Ile Gly  
865 870 875 880

Asn Lys Thr Cys Val Phe Glu Lys Glu Asn Asp Pro Thr Val Leu Arg  
885 890 895

Ser Pro Ser Ala Gly Lys Leu Thr Gln Ile Thr Val Glu Asp Gly Gly  
900 905 910

His Val Glu Ala Gly Arg Arg Tyr Ala Glu Met Glu Val Met Lys Met  
915 920 925

Ile Met Thr Leu Asn Val Gln Glu Arg Gly Arg Val Lys Tyr Ile Lys  
930 935 940

Arg Pro Gly Ala Val Leu Glu Ala Gly Cys Val Val Ala Arg Leu Glu  
945 950 955 960

Leu Asp Asp Pro Ser Lys Val His Pro Ala Glu Pro Phe Thr Gly Glu  
965 970 975

Leu Pro Ala Gln Gln Asn Thr Ala Asp Leu Gly Lys Lys Leu His Arg  
980 985 990

Val Phe His Ser Val Leu Gly Ser Leu Thr Asn Val Met Ser Gly Phe  
995 1000 1005

Cys Leu Pro Glu Pro Phe Phe Ser Ile Lys Leu Lys Glu Trp Val

1010

1015

1020

Gln Lys Leu Met Met Thr Leu Arg His Pro Ser Leu Leu Leu Asp  
1025 1030 1035

Val Gln Glu Ile Met Thr Ser Arg Ala Gly Arg Ile Pro Pro Pro  
1040 1045 1050

Val Glu Lys Ser Val Arg Lys Val Met Ala Gln Tyr Ala Ser Asn  
1055 1060 1065

Ile Thr Ser Val Leu Cys Gln Phe Pro Ser Gln Gln Ile Ala Thr  
1070 1075 1080

Ile Leu Asp Cys His Ala Ala Thr Leu Gln Arg Lys Ala Asp Arg  
1085 1090 1095

Glu Val Phe Phe Ile Asn Thr Gln Ser Met Val Gln Leu Val Gln  
1100 1105 1110

Arg Tyr Arg Ser Gly Ile Arg Gly His Met Lys Thr Val Val Ile  
1115 1120 1125

Asp Leu Leu Arg Arg Tyr Leu Arg Val Glu Thr Ile Phe Gly Lys  
1130 1135 1140

Ala Arg Asp Ala Asp Ala Asn Ser Ser Gly Met Val Gly Gly Val  
1145 1150 1155

Arg Ser Leu Ser Phe Thr Ser Val Trp Val Val Leu Ser Pro Pro  
1160 1165 1170

Ala His Tyr Asp Lys Cys Val Ile Asn Leu Arg Glu Gln Phe Lys  
1175 1180 1185

Pro Asp Met Ser Gln Val Leu Asp Cys Ile Phe Ser His Ala Gln  
1190 1195 1200

Val Thr Lys Lys Asn Gln Leu Val Ile Met Leu Ile Asp Glu Leu  
1205 1210 1215

Cys Gly Pro Asp Pro Ser Leu Ser Asp Glu Leu Ile Ser Ile Leu  
1220 1225 1230

Asn Glu Leu Thr Gln Leu Ser Lys Ser Glu His Cys Lys Val Ala  
1235 1240 1245

Leu Arg Ala Arg Gln Ile Leu Ile Ala Ser Pro Ser Tyr Glu Leu  
1250 1255 1260

Arg His Asn Gln Val Glu Ser Ile Phe Leu Ser Ala Ile Asp Met  
1265 1270 1275

Tyr Gly His Gln Phe Cys Pro Glu Asn Leu Gln Lys Leu Ile Leu  
1280 1285 1290

Ser Glu Thr Thr Ile Phe Asp Val Leu Asn Thr Phe Phe Tyr His  
1295 1300 1305

Ala Asn Lys Val Val Cys Met Ala Ser Leu Glu Val Tyr Val Gly  
1310 1315 1320

Gly Ala Tyr Ile Ala Tyr Val Leu Asn Ser Leu Gln His Arg Gln  
1325 1330 1335

Leu Pro Asp Gly Thr Cys Val Val Glu Phe Gln Phe Met Leu Pro  
1340 1345 1350

Ser Ser His Pro Asn Arg Met Thr Val Pro Ile Ser Ile Thr Asn  
1355 1360 1365

Pro Asp Leu Leu Arg His Thr Thr Glu Leu Phe Met Asp Ser Gly  
1370 1375 1380

Phe Ser Pro Leu Cys Gln Arg Met Gly Ala Met Val Ala Phe Arg  
1385 1390 1395

Arg Phe Glu Asp Phe Thr Arg Asn Phe Asp Glu Val Ile Ser Cys  
1400 1405 1410

Phe Ala Asn Val Pro Lys Asp Pro Pro Leu Phe Ser Glu Ala Arg  
1415 1420 1425

Thr Ser Leu Tyr Ser Glu Asp Asp Cys Lys Ser Leu Arg Glu Glu  
1430 1435 1440

Pro Ile His Ile Leu Asn Val Ser Ile Gln Cys Ala Asp His Leu  
1445 1450 1455

Glu Asp Glu Ala Leu Val Pro Ile Leu Arg Thr Phe Val Gln Ser  
1460 1465 1470

Lys Lys Asn Ile Leu Val Asp Tyr Gly Leu Arg Arg Ile Pro Phe  
1475 1480 1485

Leu Ile Ala Gln Glu Lys Glu Phe Pro Lys Phe Phe Thr Phe Arg  
1490 1495 1500

Ala Arg Asp Glu Phe Ala Glu Asp Arg Ile Tyr Arg His Leu Glu  
1505 1510 1515

Pro Ala Leu Ala Phe Gln Leu Glu Leu Asn Arg Met Arg Asn Phe  
1520 1525 1530

Asp Leu Thr Ala Val Pro Cys Ala Asn His Lys Met His Leu Tyr  
1535 1540 1545

Leu Gly Ala Ala Lys Val Glu Gly Arg Tyr Glu Val Thr Asp His  
1550 1555 1560

Arg Phe Phe Ile Arg Ala Ile Ile Arg His Ser Asp Leu Ile Thr  
1565 1570 1575

Lys Glu Ala Ser Phe Glu Tyr Leu Gln Asn Glu Gly Glu Arg Leu  
1580 1585 1590

Leu Leu Glu Ala Met Asp Glu Leu Glu Val Ala Phe Asn Asn Thr  
1595 1600 1605

Asn Val Arg Thr Asp Cys Asn His Ile Phe Leu Asn Phe Val Pro  
1610 1615 1620

Thr Val Ile Met Asp Pro Asn Lys Ile Glu Glu Ser Val Arg Tyr  
1625 1630 1635

Met Val Met Arg Tyr Gly Ser Arg Leu Trp Lys Leu Arg Val Leu  
1640 1645 1650

Gln Ala Glu Val Lys Ile Asn Ile Arg Gln Thr Thr Thr Gly Ser  
1655 1660 1665

Ala Val Pro Ile Arg Leu Phe Ile Thr Asn Glu Ser Gly Tyr Tyr  
1670 1675 1680

Leu Asp Ile Ser Leu Tyr Lys Glu Val Thr Asp Ser Arg Ser Gly  
1685 1690 1695

Asn Ile Met Phe His Ser Phe Gly Asn Lys Gln Gly Pro Gln His  
1700 1705 1710

Gly Met Leu Ile Asn Thr Pro Tyr Val Thr Lys Asp Leu Leu Gln  
1715 1720 1725

Ala Lys Arg Phe Gln Ala Gln Thr Leu Gly Thr Thr Tyr Ile Tyr  
1730 1735 1740

Asp Phe Pro Glu Met Phe Arg Gln Ala Leu Phe Lys Leu Trp Gly  
1745 1750 1755

Ser Pro Asp Lys Tyr Pro Lys Asp Ile Leu Thr Tyr Thr Glu Leu  
1760 1765 1770

Val Leu Asp Ser Gln Gly Gln Leu Val Glu Met Asn Arg Leu Pro  
1775 1780 1785

Gly Gly Asn Glu Val Gly Met Val Ala Phe Lys Met Arg Phe Lys  
1790 1795 1800

Thr Gln Glu Tyr Pro Glu Gly Arg Asp Val Ile Val Ile Gly Asn  
1805 1810 1815

Asp Ile Thr Phe Arg Ile Gly Ser Phe Gly Pro Gly Glu Asp Leu  
1820 1825 1830

Leu Tyr Leu Arg Ala Ser Glu Met Ala Arg Ala Glu Ala Ile Pro  
1835 1840 1845

Lys Ile Tyr Val Ala Ala Asn Ser Gly Ala Arg Ile Gly Met Ala  
1850 1855 1860

Glu Glu Ile Lys His Met Phe His Val Ala Trp Val Asp Pro Glu

1865

1870

1875

Asp Pro His Lys Gly Phe Lys Tyr Leu Tyr Leu Thr Pro Gln Asp  
1880 1885 1890

Tyr Thr Arg Ile Ser Ser Leu Asn Ser Val His Cys Lys His Ile  
1895 1900 1905

Glu Glu Gly Gly Glu Ser Arg Tyr Met Ile Thr Asp Ile Ile Gly  
1910 1915 1920

Lys Asp Asp Gly Leu Gly Val Glu Asn Leu Arg Gly Ser Gly Met  
1925 1930 1935

Ile Ala Gly Glu Ser Ser Leu Ala Tyr Glu Glu Ile Val Thr Ile  
1940 1945 1950

Ser Leu Val Thr Cys Arg Ala Ile Gly Ile Gly Ala Tyr Leu Val  
1955 1960 1965

Arg Leu Gly Gln Arg Val Ile Gln Val Glu Asn Ser His Ile Ile  
1970 1975 1980

Leu Thr Gly Ala Ser Ala Leu Asn Lys Val Leu Gly Arg Glu Val  
1985 1990 1995

Tyr Thr Ser Asn Asn Gln Leu Gly Gly Val Gln Ile Met His Tyr  
2000 2005 2010

Asn Gly Val Ser His Ile Thr Val Pro Asp Asp Phe Glu Gly Val  
2015 2020 2025

Tyr Thr Ile Leu Glu Trp Leu Ser Tyr Met Pro Lys Asp Asn His  
2030 2035 2040

Ser Pro Val Pro Ile Ile Thr Pro Thr Asp Pro Ile Asp Arg Glu  
2045 2050 2055

Ile Glu Phe Leu Pro Ser Arg Ala Pro Tyr Asp Pro Arg Trp Met  
2060 2065 2070

Leu Ala Gly Arg Pro His Pro Thr Leu Lys Gly Thr Trp Gln Ser  
2075 2080 2085

Gly Phe Phe Asp His Gly Ser Phe Lys Glu Ile Met Ala Pro Trp  
2090 2095 2100

Ala Gln Thr Val Val Thr Gly Arg Ala Arg Leu Gly Gly Ile Pro  
2105 2110 2115

Val Gly Val Ile Ala Val Glu Thr Arg Thr Val Glu Val Ala Val  
2120 2125 2130

Pro Ala Asp Pro Ala Asn Leu Asp Ser Glu Ala Lys Ile Ile Gln  
2135 2140 2145

Gln Ala Gly Gln Val Trp Phe Pro Asp Ser Ala Tyr Lys Thr Ala  
2150 2155 2160

Gln Ala Ile Lys Asp Phe Asn Arg Glu Lys Leu Pro Leu Met Ile  
2165 2170 2175

Phe Ala Asn Trp Arg Gly Phe Ser Gly Gly Met Lys Asp Met Tyr  
2180 2185 2190

Asp Gln Val Leu Lys Phe Gly Ala Tyr Ile Val Asp Gly Leu Arg  
2195 2200 2205

Gln Tyr Lys Gln Pro Ile Leu Ile Tyr Ile Arg Pro Met Arg Glu  
2210 2215 2220

Leu Arg Gly Gly Ser Trp Val Val Ile Asp Ala Thr Ile Asn Pro  
2225 2230 2235

Leu Cys Ile Glu Met Tyr Ala Asp Lys Glu Ser Arg Gly Gly Val  
2240 2245 2250

Leu Glu Pro Glu Gly Thr Val Glu Ile Lys Phe Arg Lys Glu Asp  
2255 2260 2265

Leu Ile Lys Ser Met Arg Arg Ile Asp Pro Ala Tyr Lys Lys Leu  
2270 2275 2280

Met Glu Gln Leu Gly Glu Pro Asp Leu Ser Asp Lys Asp Arg Lys  
2285 2290 2295

Asp Leu Glu Gly Arg Leu Lys Ala Arg Glu Asp Leu Leu Leu Pro  
2300 2305 2310

Ile Tyr His Gln Val Ala Val Gln Phe Ala Asp Phe His Asp Thr  
2315 2320 2325

Pro Gly Arg Met Leu Glu Lys Gly Val Ile Ser Asp Ile Leu Glu  
2330 2335 2340

Trp Lys Thr Ala Arg Thr Phe Leu Tyr Trp Arg Leu Arg Arg Leu  
2345 2350 2355

Leu Leu Glu Asp Gln Val Lys Gln Glu Ile Leu Gln Ala Ser Gly  
2360 2365 2370

Glu Leu Ser His Val His Ile Gln Ser Met Leu Arg Arg Trp Phe  
2375 2380 2385

Val Glu Thr Glu Gly Ala Val Lys Ala Tyr Leu Trp Asp Asn Asn  
2390 2395 2400

Gln Val Val Val Gln Trp Leu Glu Gln His Trp Gln Ala Gly Asp  
2405 2410 2415

Gly Pro Arg Ser Thr Ile Arg Glu Asn Ile Thr Tyr Leu Lys His  
2420 2425 2430

Asp Ser Val Leu Lys Thr Ile Arg Gly Leu Val Glu Glu Asn Pro  
2435 2440 2445

Glu Val Ala Val Asp Cys Val Ile Tyr Leu Ser Gln His Ile Ser  
2450 2455 2460

Pro Ala Glu Arg Ala Gln Val Val His Leu Leu Ser Thr Met Asp  
2465 2470 2475

Ser Pro Ala Ser Thr  
2480

<210> 5  
<211> 552  
<212> PRT  
<213> homo sapiens

<400> 5

Met Ala Glu Lys Gln Lys His Asp Gly Arg Val Lys Ile Gly His Tyr  
1 5 10 15

Val Leu Gly Asp Thr Leu Gly Val Gly Thr Phe Gly Lys Val Lys Ile  
20 25 30

Gly Glu His Gln Leu Thr Gly His Lys Val Ala Val Lys Ile Leu Asn  
35 40 45

Arg Gln Lys Ile Arg Ser Leu Asp Val Val Gly Lys Ile Lys Arg Glu  
50 55 60

Ile Gln Asn Leu Lys Leu Phe Arg His Pro His Ile Ile Lys Leu Tyr  
65 70 75 80

Gln Val Ile Ser Thr Pro Thr Asp Phe Phe Met Val Met Glu Tyr Val  
85 90 95

Ser Gly Gly Glu Leu Phe Asp Tyr Ile Cys Lys His Gly Arg Val Glu  
100 105 110

Glu Met Glu Ala Arg Arg Leu Phe Gln Gln Ile Leu Ser Ala Val Asp  
115 120 125

Tyr Cys His Arg His Met Val Val His Arg Asp Leu Lys Pro Glu Asn  
130 135 140

Val Leu Leu Asp Ala His Met Asn Ala Lys Ile Ala Asp Phe Gly Leu  
145 150 155 160

Ser Asn Met Met Ser Asp Gly Glu Phe Leu Arg Thr Ser Cys Gly Ser  
165 170 175

Pro Asn Tyr Ala Ala Pro Glu Val Ile Ser Gly Arg Leu Tyr Ala Gly  
180 185 190

Pro Glu Val Asp Ile Trp Ser Cys Gly Val Ile Leu Tyr Ala Leu Leu  
195 200 205

Cys Gly Thr Leu Pro Phe Asp Asp Glu His Val Pro Thr Leu Phe Lys  
210 215 220

Lys Ile Arg Gly Gly Val Phe Tyr Ile Pro Glu Tyr Leu Asn Arg Ser  
225 230 235 240

Val Ala Thr Leu Leu Met His Met Leu Gln Val Asp Pro Leu Lys Arg  
245 250 255

Ala Thr Ile Lys Asp Ile Arg Glu His Glu Trp Phe Lys Gln Asp Leu  
260 265 270

Pro Ser Tyr Leu Phe Pro Glu Asp Pro Ser Tyr Asp Ala Asn Val Ile  
275 280 285

Asp Asp Glu Ala Val Lys Glu Val Cys Glu Lys Phe Glu Cys Thr Glu  
290 295 300

Ser Glu Val Met Asn Ser Leu Tyr Ser Gly Asp Pro Gln Asp Gln Leu  
305 310 315 320

Ala Val Ala Tyr His Leu Ile Ile Asp Asn Arg Arg Ile Met Asn Gln  
325 330 335

Ala Ser Glu Phe Tyr Leu Ala Ser Ser Pro Pro Ser Gly Ser Phe Met  
340 345 350

Asp Asp Ser Ala Met His Ile Pro Pro Gly Leu Lys Pro His Pro Glu  
355 360 365

Arg Met Pro Pro Leu Ile Ala Asp Ser Pro Lys Ala Arg Cys Pro Leu  
370 375 380

Asp Ala Leu Asn Thr Thr Lys Pro Lys Ser Leu Ala Val Lys Lys Ala  
385 390 395 400

Lys Trp His Leu Gly Ile Arg Ser Gln Ser Lys Pro Tyr Asp Ile Met  
405 410 415

Ala Glu Val Tyr Arg Ala Met Lys Gln Leu Asp Phe Glu Trp Lys Val  
420 425 430

Val Asn Ala Tyr His Leu Arg Val Arg Arg Lys Asn Pro Val Thr Gly  
435 440 445

Asn Tyr Val Lys Met Ser Leu Gln Leu Tyr Leu Val Asp Asn Arg Ser  
450 455 460

Tyr Leu Leu Asp Phe Lys Ser Ile Asp Asp Glu Val Val Glu Gln Arg  
465 470 475 480

Ser Gly Ser Ser Thr Pro Gln Arg Ser Cys Ser Ala Ala Gly Leu His  
485 490 495

Arg Pro Arg Ser Ser Phe Asp Ser Thr Thr Ala Glu Ser His Ser Leu  
500 505 510

Ser Gly Ser Leu Thr Gly Ser Leu Thr Gly Ser Thr Leu Ser Ser Val  
515 520 525

Ser Pro Arg Leu Gly Ser His Thr Met Asp Phe Phe Glu Met Cys Ala  
530 535 540

Ser Leu Ile Thr Thr Leu Ala Arg  
545 550

<210> 6  
<211> 21  
<212> DNA  
<213> Artificial

<220>  
<223> siRNA sense strand oligonucleotide

<400> 6  
cgtgaagaag agctctgggt t 21

<210> 7  
<211> 21  
<212> DNA  
<213> Artificial

<220>  
<223> siRNA sense strand oligonucleotide

<400> 7  
gaagatggtg gagaagtgc t 21

<210> 8  
<211> 21  
<212> DNA  
<213> Artificial

<220>  
<223> siRNA sense strand oligonucleotide  
  
<400> 8  
gatgggtggag aagtgctgggt t 21

<210> 9  
<211> 21  
<212> DNA  
<213> Artificial  
  
<220>  
<223> siRNA sense strand oligonucleotide  
  
<400> 9  
gtgctggaag ctcatggact t 21

<210> 10  
<211> 21  
<212> DNA  
<213> Artificial  
  
<220>  
<223> siRNA sense strand oligonucleotide  
  
<400> 10  
gctcatggac aaggtgggtgt t 21

<210> 11  
<211> 21  
<212> DNA  
<213> Artificial  
  
<220>  
<223> siRNA sense strand oligonucleotide  
  
<400> 11  
ggtgtgcgg ttgtgtcagt t 21

<210> 12  
<211> 21  
<212> DNA  
<213> Artificial  
  
<220>  
<223> siRNA sense strand oligonucleotide  
  
<400> 12  
cccaaagctg gcgctaaagt t 21

<210> 13

<211> 21  
<212> DNA  
<213> Artificial

<220>  
<223> siRNA sense strand oligonucleotide

<400> 13  
cccaaagctg gcgctaaagt t 21

<210> 14  
<211> 21  
<212> DNA  
<213> Artificial

<220>  
<223> siRNA sense strand oligonucleotide

<400> 14  
agctggcgct aaagaatagt t 21

<210> 15  
<211> 21  
<212> DNA  
<213> Artificial

<220>  
<223> siRNA sense strand oligonucleotide

<400> 15  
agaatagccc accttatatt t 21

<210> 16  
<211> 21  
<212> DNA  
<213> Artificial

<220>  
<223> siRNA sense strand oligonucleotide

<400> 16  
tagcccacct tataatcttat t 21

<210> 17  
<211> 21  
<212> DNA  
<213> Artificial

<220>  
<223> siRNA sense strand oligonucleotide

<400> 17  
gatatgaggg gaagatggat t 21

<210> 18  
<211> 21  
<212> DNA  
<213> Artificial

<220>  
<223> siRNA sense strand oligonucleotide

<400> 18  
gatggagaca cttggagaat t 21

<210> 19  
<211> 21  
<212> DNA  
<213> Artificial

<220>  
<223> siRNA sense strand oligonucleotide

<400> 19  
ctaagcaaac cataaggcctt t 21

<210> 20  
<211> 21  
<212> DNA  
<213> Artificial

<220>  
<223> siRNA sense strand oligonucleotide

<400> 20  
gcaaaccata agcctttct t 21

<210> 21  
<211> 21  
<212> DNA  
<213> Artificial

<220>  
<223> siRNA sense strand oligonucleotide

<400> 21  
accataagcc tcttcaaggt t 21

<210> 22  
<211> 21  
<212> DNA  
<213> Artificial

<220>  
<223> siRNA sense strand oligonucleotide

<400> 22  
gcctttcaa ggaggaaat t 21

<210> 23  
<211> 21  
<212> DNA  
<213> Artificial

<220>  
<223> siRNA sense strand oligonucleotide

<400> 23  
gaaagaatgt atgaggagat t 21

<210> 24  
<211> 21  
<212> DNA  
<213> Artificial

<220>  
<223> siRNA sense strand oligonucleotide

<400> 24  
agaatgtatg aggagaattt t 21

<210> 25  
<211> 21  
<212> DNA  
<213> Artificial

<220>  
<223> siRNA sense strand oligonucleotide

<400> 25  
tgtatgagga gaattctcat t 21

<210> 26  
<211> 21  
<212> DNA  
<213> Artificial

<220>  
<223> siRNA sense strand oligonucleotide

<400> 26  
ttctcagcct aggcgaaact t 21

<210> 27  
<211> 21  
<212> DNA  
<213> Artificial

<220>  
<223> siRNA sense strand oligonucleotide

<400> 27  
acctaaccaa actgtccctt t 21

<210> 28  
<211> 21  
<212> DNA  
<213> Artificial

<220>  
<223> siRNA sense strand oligonucleotide

<400> 28  
ccaaactgtc cctcatcttt t 21

<210> 29  
<211> 21  
<212> DNA  
<213> Artificial

<220>  
<223> siRNA sense strand oligonucleotide

<400> 29  
actgtccctc atcttcagct t 21

<210> 30  
<211> 21  
<212> DNA  
<213> Artificial

<220>  
<223> siRNA sense strand oligonucleotide

<400> 30  
ggaattttc caagtggact t 21

<210> 31  
<211> 21  
<212> DNA  
<213> Artificial

<220>  
<223> siRNA sense strand oligonucleotide

<400> 31  
tctttccaag tggactcttt t 21

<210> 32

<211> 21  
<212> DNA  
<213> Artificial

<220>  
<223> siRNA sense strand oligonucleotide

<400> 32  
gtggactctt tcagggagat t 21

<210> 33  
<211> 21  
<212> DNA  
<213> Artificial

<220>  
<223> siRNA sense strand oligonucleotide

<400> 33  
agcagatgct gcggaatttt t 21

<210> 34  
<211> 21  
<212> DNA  
<213> Artificial

<220>  
<223> siRNA sense strand oligonucleotide

<400> 34  
gacaatagtc ctttggaaat t 21

<210> 35  
<211> 21  
<212> DNA  
<213> Artificial

<220>  
<223> siRNA sense strand oligonucleotide

<400> 35  
tagtcccttg gaagagcttt t 21

<210> 36  
<211> 21  
<212> DNA  
<213> Artificial

<220>  
<223> siRNA sense strand oligonucleotide

<400> 36  
gagctttcga caggctctat t 21

<210> 37  
<211> 21  
<212> DNA  
<213> Artificial

<220>  
<223> siRNA sense strand oligonucleotide

<400> 37  
gtgcatccca tcagttctgt t 21

<210> 38  
<211> 21  
<212> DNA  
<213> Artificial

<220>  
<223> siRNA sense strand oligonucleotide

<400> 38  
atccactatt gatctgacct t 21

<210> 39  
<211> 21  
<212> DNA  
<213> Artificial

<220>  
<223> siRNA sense strand oligonucleotide

<400> 39  
tttgacatct ttacccgact t 21

<210> 40  
<211> 21  
<212> DNA  
<213> Artificial

<220>  
<223> siRNA sense strand oligonucleotide

<400> 40  
ttggaacagc cttgctgtat t 21

<210> 41  
<211> 21  
<212> DNA  
<213> Artificial

<220>  
<223> siRNA sense strand oligonucleotide

<400> 41  
cagccttgct gtaactcatt t 21

<210> 42  
<211> 21  
<212> DNA  
<213> Artificial

<220>  
<223> siRNA sense strand oligonucleotide

<400> 42  
ctcatcctgg ctacatggct t 21

<210> 43  
<211> 21  
<212> DNA  
<213> Artificial

<220>  
<223> siRNA sense strand oligonucleotide

<400> 43  
gtgaaagctc ggctccagat t 21

<210> 44  
<211> 21  
<212> DNA  
<213> Artificial

<220>  
<223> siRNA sense strand oligonucleotide

<400> 44  
agctcggtc cagaaattct t 21

<210> 45  
<211> 21  
<212> DNA  
<213> Artificial

<220>  
<223> siRNA sense strand oligonucleotide

<400> 45  
attcattcac aaacctggct t 21

<210> 46  
<211> 21  
<212> DNA  
<213> Artificial

<220>  
<223> siRNA sense strand oligonucleotide  
  
<400> 46  
acctggcagt tataatcttct t 21

<210> 47  
<211> 21  
<212> DNA  
<213> Artificial  
  
<220>  
<223> siRNA sense strand oligonucleotide  
  
<400> 47  
cattctccag acaatccctt t 21

<210> 48  
<211> 21  
<212> DNA  
<213> Artificial  
  
<220>  
<223> siRNA sense strand oligonucleotide  
  
<400> 48  
tccctcacaa taaacacctt t 21

<210> 49  
<211> 21  
<212> DNA  
<213> Artificial  
  
<220>  
<223> siRNA sense strand oligonucleotide  
  
<400> 49  
taaacacctc ttccaaggcat t 21

<210> 50  
<211> 21  
<212> DNA  
<213> Artificial  
  
<220>  
<223> siRNA sense strand oligonucleotide  
  
<400> 50  
acctctcttc caagcactgt t 21

<210> 51

<211> 21  
<212> DNA  
<213> Artificial  
  
<220>  
<223> siRNA sense strand oligonucleotide  
  
<400> 51  
gcactgattg atggcttcatt t 21  
  
<210> 52  
<211> 21  
<212> DNA  
<213> Artificial  
  
<220>  
<223> siRNA sense strand oligonucleotide  
  
<400> 52  
ggcttctatt tgtttcctgt t 21  
  
<210> 53  
<211> 21  
<212> DNA  
<213> Artificial  
  
<220>  
<223> siRNA sense strand oligonucleotide  
  
<400> 53  
atcagaatcc tgatctgact t 21  
  
<210> 54  
<211> 21  
<212> DNA  
<213> Artificial  
  
<220>  
<223> siRNA sense strand oligonucleotide  
  
<400> 54  
tcctgatctg actggcttat t 21  
  
<210> 55  
<211> 21  
<212> DNA  
<213> Artificial  
  
<220>  
<223> siRNA sense strand oligonucleotide  
  
<400> 55  
ccaaactcccc aagaccatat t 21

<210> 56  
<211> 21  
<212> DNA  
<213> Artificial

<220>  
<223> siRNA sense strand oligonucleotide

<400> 56  
ctcccccaaga ccatatcaat t 21

<210> 57  
<211> 21  
<212> DNA  
<213> Artificial

<220>  
<223> siRNA sense strand oligonucleotide

<400> 57  
gaccatatca aagtgaccct t 21

<210> 58  
<211> 21  
<212> DNA  
<213> Artificial

<220>  
<223> siRNA sense strand oligonucleotide

<400> 58  
agtgaccctag gaacaatatt t 21

<210> 59  
<211> 21  
<212> DNA  
<213> Artificial

<220>  
<223> siRNA sense strand oligonucleotide

<400> 59  
caatatgaat tatactgtgt t 21

<210> 60  
<211> 21  
<212> DNA  
<213> Artificial

<220>  
<223> siRNA sense strand oligonucleotide

<400> 60  
tatgaattat actgtgagat t 21

<210> 61  
<211> 21  
<212> DNA  
<213> Artificial

<220>  
<223> siRNA sense strand oligonucleotide

<400> 61  
ttatactgtg agatgggctt t 21

<210> 62  
<211> 21  
<212> DNA  
<213> Artificial

<220>  
<223> siRNA sense strand oligonucleotide

<400> 62  
tgataaggat gtaaaagattt t 21

<210> 63  
<211> 21  
<212> DNA  
<213> Artificial

<220>  
<223> siRNA sense strand oligonucleotide

<400> 63  
ggatgtaaag attgagccct t 21

<210> 64  
<211> 21  
<212> DNA  
<213> Artificial

<220>  
<223> siRNA sense strand oligonucleotide

<400> 64  
agattgagcc ctgtggacat t 21

<210> 65  
<211> 21  
<212> DNA  
<213> Artificial

<220>  
<223> siRNA sense strand oligonucleotide  
  
<400> 65  
tcagaaggtc agggctgtct t 21

<210> 66  
<211> 21  
<212> DNA  
<213> Artificial  
  
<220>  
<223> siRNA sense strand oligonucleotide  
  
<400> 66  
ggtcagggct gtcctttctt t 21

<210> 67  
<211> 21  
<212> DNA  
<213> Artificial  
  
<220>  
<223> siRNA sense strand oligonucleotide  
  
<400> 67  
attnaaggta ctgaacccat t 21

<210> 68  
<211> 21  
<212> DNA  
<213> Artificial  
  
<220>  
<223> siRNA sense strand oligonucleotide  
  
<400> 68  
aggtaactgaa cccatcggt t 21

<210> 69  
<211> 21  
<212> DNA  
<213> Artificial  
  
<220>  
<223> siRNA sense strand oligonucleotide  
  
<400> 69  
cccatcggtgg tagatccgtt t 21

<210> 70

<211> 21  
<212> DNA  
<213> Artificial

<220>  
<223> siRNA sense strand oligonucleotide

<400> 70  
attatgatga tgatgatgat t 21

<210> 71  
<211> 21  
<212> DNA  
<213> Artificial

<220>  
<223> siRNA sense strand oligonucleotide

<400> 71  
cgagctgatg atactctctt t 21

<210> 72  
<211> 21  
<212> DNA  
<213> Artificial

<220>  
<223> siRNA sense strand oligonucleotide

<400> 72  
ggaattggct ggtgccaaat t 21

<210> 73  
<211> 21  
<212> DNA  
<213> Artificial

<220>  
<223> siRNA sense strand oligonucleotide

<400> 73  
ttggctggtg ccaagggtgg t 21

<210> 74  
<211> 21  
<212> DNA  
<213> Artificial

<220>  
<223> siRNA sense strand oligonucleotide

<400> 74  
cggccgcctt ctccattctt t 21

<210> 75  
<211> 21  
<212> DNA  
<213> Artificial

<220>  
<223> siRNA sense strand oligonucleotide

<400> 75  
gtgcttctgc tcttgaaact t 21

<210> 76  
<211> 21  
<212> DNA  
<213> Artificial

<220>  
<223> siRNA sense strand oligonucleotide

<400> 76  
ctgcttctaa ggctgcttct t 21

<210> 77  
<211> 21  
<212> DNA  
<213> Artificial

<220>  
<223> siRNA sense strand oligonucleotide

<400> 77  
ggctgcttct ggctcccttt t 21

<210> 78  
<211> 21  
<212> DNA  
<213> Artificial

<220>  
<223> siRNA sense strand oligonucleotide

<400> 78  
agacaaacca ttgccagttat t 21

<210> 79  
<211> 21  
<212> DNA  
<213> Artificial

<220>  
<223> siRNA sense strand oligonucleotide

<400> 79  
accattgccca gtacctccct t 21

<210> 80  
<211> 21  
<212> DNA  
<213> Artificial

<220>  
<223> siRNA sense strand oligonucleotide

<400> 80  
tcccgacctc aaagacgcct t 21

<210> 81  
<211> 21  
<212> DNA  
<213> Artificial

<220>  
<223> siRNA sense strand oligonucleotide

<400> 81  
agacgcccct tgccttgat t 21

<210> 82  
<211> 21  
<212> DNA  
<213> Artificial

<220>  
<223> siRNA sense strand oligonucleotide

<400> 82  
tccccaaagt accagtatct t 21

<210> 83  
<211> 21  
<212> DNA  
<213> Artificial

<220>  
<223> siRNA sense strand oligonucleotide

<400> 83  
agtaccagta tctgccccat t 21

<210> 84  
<211> 21  
<212> DNA  
<213> Artificial

<220>  
<223> siRNA sense strand oligonucleotide  
  
<400> 84  
gttccagtga tccctggact t 21

<210> 85  
<211> 21  
<212> DNA  
<213> Artificial  
  
<220>  
<223> siRNA sense strand oligonucleotide  
  
<400> 85  
gagaattaac caaccggcat t 21

<210> 86  
<211> 21  
<212> DNA  
<213> Artificial  
  
<220>  
<223> siRNA sense strand oligonucleotide  
  
<400> 86  
ttaaccaacc ggcactcact t 21

<210> 87  
<211> 21  
<212> DNA  
<213> Artificial  
  
<220>  
<223> siRNA sense strand oligonucleotide  
  
<400> 87  
ccaacccggca ctcacttcct t 21

<210> 88  
<211> 21  
<212> DNA  
<213> Artificial  
  
<220>  
<223> siRNA sense strand oligonucleotide  
  
<400> 88  
ccggcactca cttccatttt t 21

<210> 89

<211> 21  
<212> DNA  
<213> Artificial

<220>  
<223> siRNA sense strand oligonucleotide

<400> 89  
atggagccca gaccagatgt t 21

<210> 90  
<211> 21  
<212> DNA  
<213> Artificial

<220>  
<223> siRNA sense strand oligonucleotide

<400> 90  
gcacgttcag tctggatact t 21

<210> 91  
<211> 21  
<212> DNA  
<213> Artificial

<220>  
<223> siRNA sense strand oligonucleotide

<400> 91  
tagcagccca ttagtaggtt t 21

<210> 92  
<211> 21  
<212> DNA  
<213> Artificial

<220>  
<223> siRNA sense strand oligonucleotide

<400> 92  
tcaaacccttc ctcatctgct t 21

<210> 93  
<211> 21  
<212> DNA  
<213> Artificial

<220>  
<223> siRNA sense strand oligonucleotide

<400> 93  
actttcctca tctgccaatt t 21

<210> 94  
<211> 21  
<212> DNA  
<213> Artificial

<220>  
<223> siRNA sense strand oligonucleotide

<400> 94  
tgccatttat tctctggctt t 21

<210> 95  
<211> 21  
<212> DNA  
<213> Artificial

<220>  
<223> siRNA sense strand oligonucleotide

<400> 95  
ctgccacctg gggagcaatt t 21

<210> 96  
<211> 21  
<212> DNA  
<213> Artificial

<220>  
<223> siRNA sense strand oligonucleotide

<400> 96  
tgtgagggtg aagaggacat t 21

<210> 97  
<211> 21  
<212> DNA  
<213> Artificial

<220>  
<223> siRNA sense strand oligonucleotide

<400> 97  
gaggacacag agtacatgtat t 21

<210> 98  
<211> 21  
<212> DNA  
<213> Artificial

<220>  
<223> siRNA sense strand oligonucleotide

<400> 98  
gcaatgtata atattcagtt t 21

<210> 99  
<211> 21  
<212> DNA  
<213> Artificial

<220>  
<223> siRNA sense strand oligonucleotide

<400> 99  
tgtataatat tcagtcggcat t 21

<210> 100  
<211> 21  
<212> DNA  
<213> Artificial

<220>  
<223> siRNA sense strand oligonucleotide

<400> 100  
tattcagtcc caggcgccat t 21

<210> 101  
<211> 21  
<212> DNA  
<213> Artificial

<220>  
<223> siRNA sense strand oligonucleotide

<400> 101  
cactggtccc gagggagtcat t 21

<210> 102  
<211> 21  
<212> DNA  
<213> Artificial

<220>  
<223> siRNA sense strand oligonucleotide

<400> 102  
tgaggatgat gggtatgatt t 21

<210> 103  
<211> 21  
<212> DNA  
<213> Artificial

<220>  
<223> siRNA sense strand oligonucleotide  
  
<400> 103  
ctctctcaga tatctctaat t 21

<210> 104  
<211> 21  
<212> DNA  
<213> Artificial  
  
<220>  
<223> siRNA sense strand oligonucleotide  
  
<400> 104  
tgccagctcc tcctttggct t 21

<210> 105  
<211> 21  
<212> DNA  
<213> Artificial  
  
<220>  
<223> siRNA sense strand oligonucleotide  
  
<400> 105  
caaatgtcac tgaaggttct t 21

<210> 106  
<211> 21  
<212> DNA  
<213> Artificial  
  
<220>  
<223> siRNA sense strand oligonucleotide  
  
<400> 106  
atgtcactga aggttcccat t 21

<210> 107  
<211> 21  
<212> DNA  
<213> Artificial  
  
<220>  
<223> siRNA sense strand oligonucleotide  
  
<400> 107  
gttcccaag ttcccgagat t 21

<210> 108

<211> 21  
<212> DNA  
<213> Artificial  
  
<220>  
<223> siRNA sense strand oligonucleotide  
  
<400> 108  
gttcccgaga ggcctccaat t 21  
  
<210> 109  
<211> 21  
<212> DNA  
<213> Artificial  
  
<220>  
<223> siRNA sense strand oligonucleotide  
  
<400> 109  
ccattccgcg ggagaatcat t 21  
  
<210> 110  
<211> 21  
<212> DNA  
<213> Artificial  
  
<220>  
<223> siRNA sense strand oligonucleotide  
  
<400> 110  
tcaactctga acggaaagct t 21  
  
<210> 111  
<211> 21  
<212> DNA  
<213> Artificial  
  
<220>  
<223> siRNA sense strand oligonucleotide  
  
<400> 111  
ctctgaacgg aaagctggct t 21  
  
<210> 112  
<211> 21  
<212> DNA  
<213> Artificial  
  
<220>  
<223> siRNA sense strand oligonucleotide  
  
<400> 112  
cgaaaaagctg gcagctgtct t 21

<210> 113  
<211> 21  
<212> DNA  
<213> Artificial

<220>  
<223> siRNA sense strand oligonucleotide

<400> 113  
agctggcagc tgtcagcaat t 21

<210> 114  
<211> 21  
<212> DNA  
<213> Artificial

<220>  
<223> siRNA sense strand oligonucleotide

<400> 114  
cctcatgagt caggggtact t 21

<210> 115  
<211> 21  
<212> DNA  
<213> Artificial

<220>  
<223> siRNA sense strand oligonucleotide

<400> 115  
agctttggtc attgcccagt t 21

<210> 116  
<211> 21  
<212> DNA  
<213> Artificial

<220>  
<223> siRNA sense strand oligonucleotide

<400> 116  
caacatcgag atggccaaat t 21

<210> 117  
<211> 21  
<212> DNA  
<213> Artificial

<220>  
<223> siRNA sense strand oligonucleotide

<400> 117  
acatccctccg ggaatttgtt t 21

<210> 118  
<211> 21  
<212> DNA  
<213> Artificial

<220>  
<223> siRNA sense strand oligonucleotide

<400> 118  
tttggttcca tttcttctct t 21

<210> 119  
<211> 21  
<212> DNA  
<213> Artificial

<220>  
<223> siRNA sense strand oligonucleotide

<400> 119  
gtggcaccta gaagggcagt t 21

<210> 120  
<211> 21  
<212> DNA  
<213> Artificial

<220>  
<223> siRNA sense strand oligonucleotide

<400> 120  
gggcaggagg tcccttggtt t 21

<210> 121  
<211> 21  
<212> DNA  
<213> Artificial

<220>  
<223> siRNA sense strand oligonucleotide

<400> 121  
gtcttgccct ctctgtgggt t 21

<210> 122  
<211> 21  
<212> DNA  
<213> Artificial

<220>  
<223> siRNA sense strand oligonucleotide  
  
<400> 122  
gatttcaaag tggtgaaatt t 21

<210> 123  
<211> 21  
<212> DNA  
<213> Artificial  
  
<220>  
<223> siRNA sense strand oligonucleotide  
  
<400> 123  
tggagcagct agtatgtttt t 21

<210> 124  
<211> 21  
<212> DNA  
<213> Artificial  
  
<220>  
<223> siRNA antisense strand oligonucleotide  
  
<400> 124  
cccagagctc ttcttcacgt t 21

<210> 125  
<211> 21  
<212> DNA  
<213> Artificial  
  
<220>  
<223> siRNA antisense strand oligonucleotide  
  
<400> 125  
gcacttctcc accatcttct t 21

<210> 126  
<211> 21  
<212> DNA  
<213> Artificial  
  
<220>  
<223> siRNA antisense strand oligonucleotide  
  
<400> 126  
ccagcacttc tccaccatct t 21

<210> 127

<211> 21  
<212> DNA  
<213> Artificial

<220>  
<223> siRNA antisense strand oligonucleotide

<400> 127  
gtccatgagc ttccagcact t 21

<210> 128  
<211> 21  
<212> DNA  
<213> Artificial

<220>  
<223> siRNA antisense strand oligonucleotide

<400> 128  
caccaccttg tccatgagct t 21

<210> 129  
<211> 21  
<212> DNA  
<213> Artificial

<220>  
<223> siRNA antisense strand oligonucleotide

<400> 129  
ctgacacaac cgcaccacct t 21

<210> 130  
<211> 21  
<212> DNA  
<213> Artificial

<220>  
<223> siRNA antisense strand oligonucleotide

<400> 130  
cttttagcgcc agctttgggt t 21

<210> 131  
<211> 21  
<212> DNA  
<213> Artificial

<220>  
<223> siRNA antisense strand oligonucleotide

<400> 131  
cttttagcgcc agctttgggt t 21

<210> 132  
<211> 21  
<212> DNA  
<213> Artificial

<220>  
<223> siRNA antisense strand oligonucleotide

<400> 132  
ctattcttta gcgccagctt t 21

<210> 133  
<211> 21  
<212> DNA  
<213> Artificial

<220>  
<223> siRNA antisense strand oligonucleotide

<400> 133  
atataagggtg ggctattctt t 21

<210> 134  
<211> 21  
<212> DNA  
<213> Artificial

<220>  
<223> siRNA antisense strand oligonucleotide

<400> 134  
taagatataaa ggtgggctat t 21

<210> 135  
<211> 21  
<212> DNA  
<213> Artificial

<220>  
<223> siRNA antisense strand oligonucleotide

<400> 135  
tccatcttcc cctcatatct t 21

<210> 136  
<211> 21  
<212> DNA  
<213> Artificial

<220>  
<223> siRNA antisense strand oligonucleotide

<400> 136  
ttctccaagt gtctccatct t 21

<210> 137  
<211> 21  
<212> DNA  
<213> Artificial  
  
<220>  
<223> siRNA antisense strand oligonucleotide

<400> 137  
aggcttatgg tttgcttagt t 21

<210> 138  
<211> 21  
<212> DNA  
<213> Artificial  
  
<220>  
<223> siRNA antisense strand oligonucleotide

<400> 138  
gaagaggctt atggtttgct t 21

<210> 139  
<211> 21  
<212> DNA  
<213> Artificial  
  
<220>  
<223> siRNA antisense strand oligonucleotide

<400> 139  
ccttgaagag gcttatggtt t 21

<210> 140  
<211> 21  
<212> DNA  
<213> Artificial  
  
<220>  
<223> siRNA antisense strand oligonucleotide

<400> 140  
tttccctcct tgaagaggct t 21

<210> 141  
<211> 21  
<212> DNA  
<213> Artificial

<220>  
<223> siRNA antisense strand oligonucleotide  
  
<400> 141  
tctcctcata cattcttct t 21

<210> 142  
<211> 21  
<212> DNA  
<213> Artificial  
  
<220>  
<223> siRNA antisense strand oligonucleotide  
  
<400> 142  
aattctccctc atacattctt t 21

<210> 143  
<211> 21  
<212> DNA  
<213> Artificial  
  
<220>  
<223> siRNA antisense strand oligonucleotide  
  
<400> 143  
tgagaattct cctcatacat t 21

<210> 144  
<211> 21  
<212> DNA  
<213> Artificial  
  
<220>  
<223> siRNA antisense strand oligonucleotide  
  
<400> 144  
gtttcgccata ggctgagaat t 21

<210> 145  
<211> 21  
<212> DNA  
<213> Artificial  
  
<220>  
<223> siRNA antisense strand oligonucleotide  
  
<400> 145  
aggacagtt tggtaggtt t 21

<210> 146

<211> 21  
<212> DNA  
<213> Artificial

<220>  
<223> siRNA antisense strand oligonucleotide

<400> 146  
aagatgaggg acagtttggt t 21

<210> 147  
<211> 21  
<212> DNA  
<213> Artificial

<220>  
<223> siRNA antisense strand oligonucleotide

<400> 147  
gctgaagatg agggacagtt t 21

<210> 148  
<211> 21  
<212> DNA  
<213> Artificial

<220>  
<223> siRNA antisense strand oligonucleotide

<400> 148  
gtccacttgg aaagattcct t 21

<210> 149  
<211> 21  
<212> DNA  
<213> Artificial

<220>  
<223> siRNA antisense strand oligonucleotide

<400> 149  
aagagtccac ttggaaagat t 21

<210> 150  
<211> 21  
<212> DNA  
<213> Artificial

<220>  
<223> siRNA antisense strand oligonucleotide

<400> 150  
tctccctgaa agagtccact t 21

<210> 151  
<211> 21  
<212> DNA  
<213> Artificial

<220>  
<223> siRNA antisense strand oligonucleotide

<400> 151  
aaattccgca gcatctgctt t 21

<210> 152  
<211> 21  
<212> DNA  
<213> Artificial

<220>  
<223> siRNA antisense strand oligonucleotide

<400> 152  
cttccaaggg actattgtct t 21

<210> 153  
<211> 21  
<212> DNA  
<213> Artificial

<220>  
<223> siRNA antisense strand oligonucleotide

<400> 153  
aagctttcc aaggactat t 21

<210> 154  
<211> 21  
<212> DNA  
<213> Artificial

<220>  
<223> siRNA antisense strand oligonucleotide

<400> 154  
tagagcctgt cgaaagctct t 21

<210> 155  
<211> 21  
<212> DNA  
<213> Artificial

<220>  
<223> siRNA antisense strand oligonucleotide

<400> 155  
cagaactgat gggatgcact t 21

<210> 156  
<211> 21  
<212> DNA  
<213> Artificial

<220>  
<223> siRNA antisense strand oligonucleotide

<400> 156  
ggtcagatca atagtggatt t 21

<210> 157  
<211> 21  
<212> DNA  
<213> Artificial

<220>  
<223> siRNA antisense strand oligonucleotide

<400> 157  
gtcgggtaaa gatgtcaaat t 21

<210> 158  
<211> 21  
<212> DNA  
<213> Artificial

<220>  
<223> siRNA antisense strand oligonucleotide

<400> 158  
tacagcaagg ctgttccaaat t 21

<210> 159  
<211> 21  
<212> DNA  
<213> Artificial

<220>  
<223> siRNA antisense strand oligonucleotide

<400> 159  
atgagttaca gcaaggctgt t 21

<210> 160  
<211> 21  
<212> DNA  
<213> Artificial

<220>  
<223> siRNA antisense strand oligonucleotide

<400> 160  
gccatgtagc caggatgagt t 21

<210> 161  
<211> 21  
<212> DNA  
<213> Artificial

<220>  
<223> siRNA antisense strand oligonucleotide

<400> 161  
tctggagccg agctttcact t 21

<210> 162  
<211> 21  
<212> DNA  
<213> Artificial

<220>  
<223> siRNA antisense strand oligonucleotide

<400> 162  
gaatttctgg agccgagctt t 21

<210> 163  
<211> 21  
<212> DNA  
<213> Artificial

<220>  
<223> siRNA antisense strand oligonucleotide

<400> 163  
gccaggttg tgaatgaatt t 21

<210> 164  
<211> 21  
<212> DNA  
<213> Artificial

<220>  
<223> siRNA antisense strand oligonucleotide

<400> 164  
gaagatataa ctgccagggtt t 21

<210> 165

<211> 21  
<212> DNA  
<213> Artificial

<220>  
<223> siRNA antisense strand oligonucleotide

<400> 165  
agggattgtc tggagaatgt t 21

<210> 166  
<211> 21  
<212> DNA  
<213> Artificial

<220>  
<223> siRNA antisense strand oligonucleotide

<400> 166  
agaggtttat tgtgagggat t 21

<210> 167  
<211> 21  
<212> DNA  
<213> Artificial

<220>  
<223> siRNA antisense strand oligonucleotide

<400> 167  
tgcttggaaag agaggtttat t 21

<210> 168  
<211> 21  
<212> DNA  
<213> Artificial

<220>  
<223> siRNA antisense strand oligonucleotide

<400> 168  
cagtgcgg aagagaggtt t 21

<210> 169  
<211> 21  
<212> DNA  
<213> Artificial

<220>  
<223> siRNA antisense strand oligonucleotide

<400> 169  
tgaagccatc aatcagtgt t 21

<210> 170  
<211> 21  
<212> DNA  
<213> Artificial

<220>  
<223> siRNA antisense strand oligonucleotide

<400> 170  
cagggaaacaa atagaaggcct t 21

<210> 171  
<211> 21  
<212> DNA  
<213> Artificial

<220>  
<223> siRNA antisense strand oligonucleotide

<400> 171  
gtcagatcag gattctgatt t 21

<210> 172  
<211> 21  
<212> DNA  
<213> Artificial

<220>  
<223> siRNA antisense strand oligonucleotide

<400> 172  
taagccagtc agatcaggat t 21

<210> 173  
<211> 21  
<212> DNA  
<213> Artificial

<220>  
<223> siRNA antisense strand oligonucleotide

<400> 173  
tatggtcttg gggagttgggt t 21

<210> 174  
<211> 21  
<212> DNA  
<213> Artificial

<220>  
<223> siRNA antisense strand oligonucleotide

<400> 174  
ttgatatgg tttggggagt t 21

<210> 175  
<211> 21  
<212> DNA  
<213> Artificial

<220>  
<223> siRNA antisense strand oligonucleotide

<400> 175  
gggtcactt gatatggtct t 21

<210> 176  
<211> 21  
<212> DNA  
<213> Artificial

<220>  
<223> siRNA antisense strand oligonucleotide

<400> 176  
atattgttcc tgggtcactt t 21

<210> 177  
<211> 21  
<212> DNA  
<213> Artificial

<220>  
<223> siRNA antisense strand oligonucleotide

<400> 177  
cacagtataa ttcatattgt t 21

<210> 178  
<211> 21  
<212> DNA  
<213> Artificial

<220>  
<223> siRNA antisense strand oligonucleotide

<400> 178  
tctcacagta taattcatat t 21

<210> 179  
<211> 21  
<212> DNA  
<213> Artificial

<220>  
<223> siRNA antisense strand oligonucleotide  
  
<400> 179  
agcccatctc acagtataat t 21

<210> 180  
<211> 21  
<212> DNA  
<213> Artificial  
  
<220>  
<223> siRNA antisense strand oligonucleotide  
  
<400> 180  
aatcttaca tccttatcat t 21

<210> 181  
<211> 21  
<212> DNA  
<213> Artificial  
  
<220>  
<223> siRNA antisense strand oligonucleotide  
  
<400> 181  
gggctcaatc tttacatcct t 21

<210> 182  
<211> 21  
<212> DNA  
<213> Artificial  
  
<220>  
<223> siRNA antisense strand oligonucleotide  
  
<400> 182  
tgtccacagg gctcaatctt t 21

<210> 183  
<211> 21  
<212> DNA  
<213> Artificial  
  
<220>  
<223> siRNA antisense strand oligonucleotide  
  
<400> 183  
gacagccctg accttctgat t 21

<210> 184

<211> 21  
<212> DNA  
<213> Artificial

<220>  
<223> siRNA antisense strand oligonucleotide

<400> 184  
agaaaaggaca gccctgaccc t 21

<210> 185  
<211> 21  
<212> DNA  
<213> Artificial

<220>  
<223> siRNA antisense strand oligonucleotide

<400> 185  
tgggttcagt acctttaatt t 21

<210> 186  
<211> 21  
<212> DNA  
<213> Artificial

<220>  
<223> siRNA antisense strand oligonucleotide

<400> 186  
cacgatgggt tcagtagcc t 21

<210> 187  
<211> 21  
<212> DNA  
<213> Artificial

<220>  
<223> siRNA antisense strand oligonucleotide

<400> 187  
acggatctac cacgatgggt t 21

<210> 188  
<211> 21  
<212> DNA  
<213> Artificial

<220>  
<223> siRNA antisense strand oligonucleotide

<400> 188  
tcatcatcat catcataatt t 21

<210> 189  
<211> 21  
<212> DNA  
<213> Artificial

<220>  
<223> siRNA antisense strand oligonucleotide

<400> 189  
agagagtatc atcagctcgt t 21

<210> 190  
<211> 21  
<212> DNA  
<213> Artificial

<220>  
<223> siRNA antisense strand oligonucleotide

<400> 190  
cttggcacca gccaattcct t 21

<210> 191  
<211> 21  
<212> DNA  
<213> Artificial

<220>  
<223> siRNA antisense strand oligonucleotide

<400> 191  
ccacaccttggc accagccaat t 21

<210> 192  
<211> 21  
<212> DNA  
<213> Artificial

<220>  
<223> siRNA antisense strand oligonucleotide

<400> 192  
agaatggaga aggcggccgt t 21

<210> 193  
<211> 21  
<212> DNA  
<213> Artificial

<220>  
<223> siRNA antisense strand oligonucleotide

<400> 193  
gttccaagag cagaaggact t

21

<210> 194  
<211> 21  
<212> DNA  
<213> Artificial  
  
<220>  
<223> siRNA antisense strand oligonucleotide

<400> 194  
gaagcagcct tagaaggagt t

21

<210> 195  
<211> 21  
<212> DNA  
<213> Artificial  
  
<220>  
<223> siRNA antisense strand oligonucleotide

<400> 195  
aagggagcca gaaggcgcct t

21

<210> 196  
<211> 21  
<212> DNA  
<213> Artificial  
  
<220>  
<223> siRNA antisense strand oligonucleotide

<400> 196  
tactggaat ggtttgtctt t

21

<210> 197  
<211> 21  
<212> DNA  
<213> Artificial  
  
<220>  
<223> siRNA antisense strand oligonucleotide

<400> 197  
gggaggtact ggcaatggtt t

21

<210> 198  
<211> 21  
<212> DNA  
<213> Artificial

<220>  
<223> siRNA antisense strand oligonucleotide  
  
<400> 198  
ggcgtcttg aggtcggtt t 21

<210> 199  
<211> 21  
<212> DNA  
<213> Artificial  
  
<220>  
<223> siRNA antisense strand oligonucleotide  
  
<400> 199  
tacaaggcaa ggggcgtctt t 21

<210> 200  
<211> 21  
<212> DNA  
<213> Artificial  
  
<220>  
<223> siRNA antisense strand oligonucleotide  
  
<400> 200  
gatactggta ctttgggtt t 21

<210> 201  
<211> 21  
<212> DNA  
<213> Artificial  
  
<220>  
<223> siRNA antisense strand oligonucleotide  
  
<400> 201  
tggggcagat actggtaact t 21

<210> 202  
<211> 21  
<212> DNA  
<213> Artificial  
  
<220>  
<223> siRNA antisense strand oligonucleotide  
  
<400> 202  
gtccaggat cactggaact t 21

<210> 203

<211> 21  
<212> DNA  
<213> Artificial

<220>  
<223> siRNA antisense strand oligonucleotide

<400> 203  
tgccgggtgg ttaattctct t 21

<210> 204  
<211> 21  
<212> DNA  
<213> Artificial

<220>  
<223> siRNA antisense strand oligonucleotide

<400> 204  
gtgagtgccg gttggtaat t 21

<210> 205  
<211> 21  
<212> DNA  
<213> Artificial

<220>  
<223> siRNA antisense strand oligonucleotide

<400> 205  
ggaagtgagt gccgggttgt t 21

<210> 206  
<211> 21  
<212> DNA  
<213> Artificial

<220>  
<223> siRNA antisense strand oligonucleotide

<400> 206  
aatggaaagt gagtgccggt t 21

<210> 207  
<211> 21  
<212> DNA  
<213> Artificial

<220>  
<223> siRNA antisense strand oligonucleotide

<400> 207  
catctggtct gggctccatt t 21

<210> 208  
<211> 21  
<212> DNA  
<213> Artificial

<220>  
<223> siRNA antisense strand oligonucleotide

<400> 208  
gtatccagac tgaacgtgct t 21

<210> 209  
<211> 21  
<212> DNA  
<213> Artificial

<220>  
<223> siRNA antisense strand oligonucleotide

<400> 209  
acctactaat gggctgctat t 21

<210> 210  
<211> 21  
<212> DNA  
<213> Artificial

<220>  
<223> siRNA antisense strand oligonucleotide

<400> 210  
gcagatgagg aaggtttgat t 21

<210> 211  
<211> 21  
<212> DNA  
<213> Artificial

<220>  
<223> siRNA antisense strand oligonucleotide

<400> 211  
attggcagat gaggaaggtt t 21

<210> 212  
<211> 21  
<212> DNA  
<213> Artificial

<220>  
<223> siRNA antisense strand oligonucleotide

<400> 212  
agccagagaa taaatggcat t 21

<210> 213  
<211> 21  
<212> DNA  
<213> Artificial

<220>  
<223> siRNA antisense strand oligonucleotide

<400> 213  
attgctcccc aggtggcagt t 21

<210> 214  
<211> 21  
<212> DNA  
<213> Artificial

<220>  
<223> siRNA antisense strand oligonucleotide

<400> 214  
tgtcctcttc accctcacat t 21

<210> 215  
<211> 21  
<212> DNA  
<213> Artificial

<220>  
<223> siRNA antisense strand oligonucleotide

<400> 215  
tcatgtactc tgtgtcctct t 21

<210> 216  
<211> 21  
<212> DNA  
<213> Artificial

<220>  
<223> siRNA antisense strand oligonucleotide

<400> 216  
actgaatatt atacattgct t 21

<210> 217  
<211> 21  
<212> DNA  
<213> Artificial

<220>  
<223> siRNA antisense strand oligonucleotide  
  
<400> 217  
tgggactgaa tattatacat t 21

<210> 218  
<211> 21  
<212> DNA  
<213> Artificial  
  
<220>  
<223> siRNA antisense strand oligonucleotide  
  
<400> 218  
tggcgccctgg gactgaatat t 21

<210> 219  
<211> 21  
<212> DNA  
<213> Artificial  
  
<220>  
<223> siRNA antisense strand oligonucleotide  
  
<400> 219  
tgactcctcg ggaccagtgt t 21

<210> 220  
<211> 21  
<212> DNA  
<213> Artificial  
  
<220>  
<223> siRNA antisense strand oligonucleotide  
  
<400> 220  
atcataccctt tcatcctcat t 21

<210> 221  
<211> 21  
<212> DNA  
<213> Artificial  
  
<220>  
<223> siRNA antisense strand oligonucleotide  
  
<400> 221  
tttagagatat ctgagagagt t 21

<210> 222

<211> 21  
<212> DNA  
<213> Artificial

<220>  
<223> siRNA antisense strand oligonucleotide

<400> 222  
gccaaaaggag gagctggcat t 21

<210> 223  
<211> 21  
<212> DNA  
<213> Artificial

<220>  
<223> siRNA antisense strand oligonucleotide

<400> 223  
gaaccttcag tgacatttgc t 21

<210> 224  
<211> 21  
<212> DNA  
<213> Artificial

<220>  
<223> siRNA antisense strand oligonucleotide

<400> 224  
tgggaacctt cagtgcacatt t 21

<210> 225  
<211> 21  
<212> DNA  
<213> Artificial

<220>  
<223> siRNA antisense strand oligonucleotide

<400> 225  
tctcggaac ttgggaacct t 21

<210> 226  
<211> 21  
<212> DNA  
<213> Artificial

<220>  
<223> siRNA antisense strand oligonucleotide

<400> 226  
ttggaggcct ctcggaaact t 21

<210> 227  
<211> 21  
<212> DNA  
<213> Artificial

<220>  
<223> siRNA antisense strand oligonucleotide

<400> 227  
tgattctccg cgggaaatgg t 21

<210> 228  
<211> 21  
<212> DNA  
<213> Artificial

<220>  
<223> siRNA antisense strand oligonucleotide

<400> 228  
gcttccgtt cagagttgat t 21

<210> 229  
<211> 21  
<212> DNA  
<213> Artificial

<220>  
<223> siRNA antisense strand oligonucleotide

<400> 229  
gccagcttcc cgttcagagt t 21

<210> 230  
<211> 21  
<212> DNA  
<213> Artificial

<220>  
<223> siRNA antisense strand oligonucleotide

<400> 230  
gacagctgcc agctttccgt t 21

<210> 231  
<211> 21  
<212> DNA  
<213> Artificial

<220>  
<223> siRNA antisense strand oligonucleotide

<400> 231  
ttgctgacag ctgccagctt t 21

<210> 232  
<211> 21  
<212> DNA  
<213> Artificial

<220>  
<223> siRNA antisense strand oligonucleotide

<400> 232  
gtacccctga ctcatgaggt t 21

<210> 233  
<211> 21  
<212> DNA  
<213> Artificial

<220>  
<223> siRNA antisense strand oligonucleotide

<400> 233  
ctgggcaatg accaaagctt t 21

<210> 234  
<211> 21  
<212> DNA  
<213> Artificial

<220>  
<223> siRNA antisense strand oligonucleotide

<400> 234  
tttggccatc tcgatgttgt t 21

<210> 235  
<211> 21  
<212> DNA  
<213> Artificial

<220>  
<223> siRNA antisense strand oligonucleotide

<400> 235  
acaattcccc ggaggatgtt t 21

<210> 236  
<211> 21  
<212> DNA  
<213> Artificial

<220>  
<223> siRNA antisense strand oligonucleotide

<400> 236  
gagaagaaat ggaaacaaat t

21

<210> 237  
<211> 21  
<212> DNA  
<213> Artificial

<220>  
<223> siRNA antisense strand oligonucleotide  
<400> 237  
ctgcccttct aggtgccact t

21

<210> 238  
<211> 21  
<212> DNA  
<213> Artificial

<220>  
<223> siRNA antisense strand oligonucleotide  
<400> 238  
accaaaggaa ctcctgccct t

21

<210> 239  
<211> 21  
<212> DNA  
<213> Artificial

<220>  
<223> siRNA antisense strand oligonucleotide  
<400> 239  
cccacagaga gggcaagact t

21

<210> 240  
<211> 21  
<212> DNA  
<213> Artificial

<220>  
<223> siRNA antisense strand oligonucleotide  
<400> 240  
atttcaccac ttgtaaatct t

21

<210> 241

<211> 21  
<212> DNA  
<213> Artificial

<220>  
<223> siRNA antisense strand oligonucleotide

<400> 241  
aaacatacta gctgctccat t 21

<210> 242  
<211> 3  
<212> DNA  
<213> Artificial

<220>  
<223> shRNA loop sequence

<400> 242  
ccc 3

<210> 243  
<211> 4  
<212> DNA  
<213> Artificial

<220>  
<223> shRNA loop sequence

<400> 243  
ttcg 4

<210> 244  
<211> 5  
<212> DNA  
<213> Artificial

<220>  
<223> shRNA loop sequence

<400> 244  
ccacc 5

<210> 245  
<211> 6  
<212> DNA  
<213> Artificial

<220>  
<223> shRNA loop sequence

<400> 245  
ctcgag 6

<210> 246  
<211> 6  
<212> DNA  
<213> Artificial  
  
<220>  
<223> shRNA loop sequence  
  
<400> 246  
aagctt

6

<210> 247  
<211> 7  
<212> DNA  
<213> Artificial  
  
<220>  
<223> shRNA loop sequence  
  
<400> 247  
ccacacc

7

<210> 248  
<211> 9  
<212> DNA  
<213> Artificial  
  
<220>  
<223> shRNA loop sequence  
  
<400> 248  
ttcaagaga

9

<210> 249  
<211> 2721  
<212> DNA  
<213> Artificial  
  
<220>  
<223> c-Cbl G306E

<220>  
<221> CDS  
<222> (1)..(2718)

<400> 249  
atg gcc ggc aac gtg aag aag agc tct ggg gcc ggg ggc ggc acg ggc  
Met Ala Gly Asn Val Lys Lys Ser Ser Gly Ala Gly Gly Gly Thr Gly  
1 5 10 15

48

tcc ggg ggc tcg ggt tcg ggt ggc ctg att ggg ctc atg aag gac gcc

96

Ser	Gly	Gly	Ser	Gly	Gly	Leu	Ile	Gly	Leu	Met	Lys	Asp	Ala	
20					25					30				
ttc cag ccg cac cac cac cac cac ctc agc ccc cac ccg ccg													144	
Phe	Gln	Pro	His	Leu	Ser	Pro	His	Pro						
35										40				45
ggg acg gtg gac aag aag atg gtg gag aag tgc tgg aag ctc atg gac													192	
Gly	Thr	Val	Asp	Lys	Lys	Met	Val	Glu	Lys	Cys	Trp	Lys	Leu	Met
50										55				60
aag gtg gtg cgg ttg tgt cag aac cca aag ctg gcg cta aag aat agc													240	
Lys	Val	Val	Arg	Leu	Cys	Gln	Asn	Pro	Lys	Leu	Ala	Leu	Lys	Asn
65										70				80
cca cct tat atc tta gac ctg cta cca gat acc tac cag cat ctc cgt													288	
Pro	Pro	Tyr	Ile	Leu	Asp	Leu	Leu	Pro	Asp	Thr	Tyr	Gln	His	Leu
85										90				95
act atc ttg tca aga tat gag ggg aag atg gag aca ctt gga gaa aat													336	
Thr	Ile	Leu	Ser	Arg	Tyr	Glu	Gly	Lys	Met	Glu	Thr	Leu	Gly	Glu
100										105				110
gag tat ttt agg gtg ttt atg gag aat ttg atg aag aaa act aag caa													384	
Glu	Tyr	Phe	Arg	Val	Phe	Met	Glu	Asn	Leu	Met	Lys	Thr	Lys	Gln
115										120				125
acc ata agc ctc ttc aag gag gga aaa gaa aga atg tat gag gag aat													432	
Thr	Ile	Ser	Leu	Phe	Lys	Glu	Gly	Lys	Glu	Arg	Met	Tyr	Glu	Asn
130										135				140
tct cag cct agg cga aac cta acc aaa ctg tcc ctc atc ttc agc cac													480	
Ser	Gln	Pro	Arg	Arg	Asn	Leu	Thr	Lys	Leu	Ser	Leu	Ile	Phe	Ser
145										150				160
atg ctg gca gaa cta aaa gga atc ttt cca agt gga ctc ttt cag gga													528	
Met	Leu	Ala	Glu	Leu	Lys	Gly	Ile	Phe	Pro	Ser	Gly	Leu	Phe	Gln
165										170				175
gac aca ttt cgg att act aaa gca gat gct gcg gaa ttt tgg aga aaa													576	
Asp	Thr	Phe	Arg	Ile	Thr	Lys	Ala	Asp	Ala	Ala	Glu	Phe	Trp	Arg
180										185				190
gct ttt ggg gaa aag aca ata gtc cct tgg aag agc ttt cga cag gct													624	
Ala	Phe	Gly	Glu	Lys	Thr	Ile	Val	Pro	Trp	Lys	Ser	Phe	Arg	Gln
195										200				205
cta cat gaa gtg cat ccc atc agt tct ggg ctg gag gcc atg gct ctg													672	
Leu	His	Glu	Val	His	Pro	Ile	Ser	Ser	Gly	Leu	Glu	Ala	Met	Ala
210										215				220
aaa tcc act att gat ctg acc tgc aat gat tat att tcg gtt ttt gaa													720	
Lys	Ser	Thr	Ile	Asp	Leu	Thr	Cys	Asn	Asp	Tyr	Ile	Ser	Val	Phe
225										230				240
ttt gac atc ttt acc cga ctc ttt cag ccc tgg tcc tct ttg ctc agg													768	
Phe	Asp	Ile	Phe	Thr	Arg	Leu	Phe	Gln	Pro	Trp	Ser	Ser	Leu	Leu

245	250	255	
aat tgg aac agc ctt gct gta act cat cct ggc tac atg gct ttt ttg Asn Trp Asn Ser Leu Ala Val Thr His Pro Gly Tyr Met Ala Phe Leu 260	265	270	816
acg tat gac gaa gtg aaa gct cgg ctc cag aaa ttc att cac aaa cct Thr Tyr Asp Glu Val Lys Ala Arg Leu Gln Lys Phe Ile His Lys Pro 275	280	285	864
ggc agt tat atc ttc cgg ctg agc tgt act cgt ctg ggt cag tgg gct Gly Ser Tyr Ile Phe Arg Leu Ser Cys Thr Arg Leu Gly Gln Trp Ala 290	295	300	912
att gag tat gtt act gct gat ggg aac att ctc cag aca atc cct cac Ile Glu Tyr Val Thr Ala Asp Gly Asn Ile Leu Gln Thr Ile Pro His 305	310	315	960
aat aaa cct ctc ttccaa gca ctg att gat ggc ttc agg gaa ggc ttc Asn Lys Pro Leu Phe Gln Ala Leu Ile Asp Gly Phe Arg Glu Gly Phe 325	330	335	1008
tat ttg ttt cct gat gga cga aat cag aat cct gat ctg act ggc tta Tyr Leu Phe Pro Asp Gly Arg Asn Gln Asn Pro Asp Leu Thr Gly Leu 340	345	350	1056
tgt gaa cca act ccc caa gac cat atc aaa gtg acc cag gaa caa tat Cys Glu Pro Thr Pro Gln Asp His Ile Lys Val Thr Gln Glu Gln Tyr 355	360	365	1104
gaa tta tac tgt gag atg ggc tcc aca ttc caa cta tgt aaa ata tgt Glu Leu Tyr Cys Glu Met Gly Ser Thr Phe Gln Leu Cys Lys Ile Cys 370	375	380	1152
gct gaa aat gat aag gat gta aag att gag ccc tgt gga cac ctc atg Ala Glu Asn Asp Lys Asp Val Lys Ile Glu Pro Cys Gly His Leu Met 385	390	395	1200
tgc aca tcc tgt ctt aca tcc tgg cag gaa tca gaa ggt cag ggc tgt Cys Thr Ser Cys Leu Thr Ser Trp Gln Glu Ser Glu Gly Gln Gly Cys 405	410	415	1248
cct ttc tgc cga tgt gaa att aaa ggt act gaa ccc atc gtg gta gat Pro Phe Cys Arg Cys Glu Ile Lys Gly Thr Glu Pro Ile Val Val Asp 420	425	430	1296
ccg ttt gat cct aga ggg agt ggc agc ctg ttg agg caa gga gca gag Pro Phe Asp Pro Arg Gly Ser Gly Ser Leu Leu Arg Gln Gly Ala Glu 435	440	445	1344
gga gct ccc tcc cca aat tat gat gat gat gat gaa cga gct gat Gly Ala Pro Ser Pro Asn Tyr Asp Asp Asp Asp Glu Arg Ala Asp 450	455	460	1392
gat act ctc ttc atg atg aag gaa ttg gct ggt gcc aag gtg gaa cgg Asp Thr Leu Phe Met Met Lys Glu Leu Ala Gly Ala Lys Val Glu Arg 465	470	475	1440

ccg cct tct cca ttc tcc atg gcc cca caa gct tcc ctt ccc ccg gtg Pro Pro Ser Pro Phe Ser Met Ala Pro Gln Ala Ser Leu Pro Pro Val 485 490 495	1488
cca cca cga ctt gac ctt ctg ccg cag cga gta tgt gtt ccc tca agt Pro Pro Arg Leu Asp Leu Leu Pro Gln Arg Val Cys Val Pro Ser Ser 500 505 510	1536
gct tct gct ctt gga act gct tct aag gct gct tct ggc tcc ctt cat Ala Ser Ala Leu Gly Thr Ala Ser Lys Ala Ala Ser Gly Ser Leu His 515 520 525	1584
aaa gac aaa cca ttg cca gta cct ccc aca ctt cga gat ctt cca cca Lys Asp Lys Pro Leu Pro Val Pro Pro Thr Leu Arg Asp Leu Pro Pro 530 535 540	1632
cca ccg cct cca gac cgg cca tat tct gtt gga gca gaa tcc cga cct Pro Pro Pro Pro Asp Arg Pro Tyr Ser Val Gly Ala Glu Ser Arg Pro 545 550 555 560	1680
caa aga cgc ccc ttg cct tgt aca cca ggc gac tgt ccc tcc aga gac Gln Arg Arg Pro Leu Pro Cys Thr Pro Gly Asp Cys Pro Ser Arg Asp 565 570 575	1728
aaa ctg ccc cct gtc ccc tct agc cgc ctt gga gac tca tgg ctg ccc Lys Leu Pro Pro Val Pro Ser Ser Arg Leu Gly Asp Ser Trp Leu Pro 580 585 590	1776
cg <sup>g</sup> cca atc, ccc aaa gta cca gta tct gcc cca agt tcc agt gat ccc Arg Pro Ile Pro Lys Val Pro Val Ser Ala Pro Ser Ser Asp Pro 595 600 605	1824
tgg aca gga aga gaa tta acc aac cgg cac tca ctt cca ttt tca ttg Trp Thr Gly Arg Glu Leu Thr Asn Arg His Ser Leu Pro Phe Ser Leu 610 615 620	1872
ccc tca caa atg gag ccc aga cca gat gtg cct agg ctc gga agc acg Pro Ser Gln Met Glu Pro Arg Pro Asp Val Pro Arg Leu Gly Ser Thr 625 630 635 640	1920
ttc agt ctg gat acc tcc atg agt atg aat agc agc cca tta gta ggt Phe Ser Leu Asp Thr Ser Met Ser Met Asn Ser Ser Pro Leu Val Gly 645 650 655	1968
cca gag tgt gac cac ccc aaa atc aaa cct tcc tca tct gcc aat gcc Pro Glu Cys Asp His Pro Lys Ile Lys Pro Ser Ser Ser Ala Asn Ala 660 665 670	2016
att tat tct ctg gct gcc aga cct ctt cct gtg cca aaa ctg cca cct Ile Tyr Ser Leu Ala Ala Arg Pro Leu Pro Val Pro Lys Leu Pro Pro 675 680 685	2064
ggg gag caa tgt gag ggt gaa gag gac aca gag tac atg act ccc tct Gly Glu Gln Cys Glu Gly Glu Glu Asp Thr Glu Tyr Met Thr Pro Ser 690 695 700	2112

tcc agg cct cta cgg cct ttg gat aca tcc cag agt tca cga gca tgt Ser Arg Pro Leu Arg Pro Leu Asp Thr Ser Gln Ser Ser Arg Ala Cys 705 710 715 720	2160
gat tgc gac cag cag att gat agc tgt acg tat gaa gca atg tat aat Asp Cys Asp Gln Gln Ile Asp Ser Cys Thr Tyr Glu Ala Met Tyr Asn 725 730 735	2208
att cag tcc cag gcg cca tct atc acc gag agc agc acc ttt ggt gaa Ile Gln Ser Gln Ala Pro Ser Ile Thr Glu Ser Ser Thr Phe Gly Glu 740 745 750	2256
ggg aat ttg gcc gca gcc cat gcc aac act ggt ccc gag gag tca gaa Gly Asn Leu Ala Ala His Ala Asn Thr Gly Pro Glu Glu Ser Glu 755 760 765	2304
aat gag gat gat ggg tat gat gtc cca aag cca cct gtg ccg gcc gtg Asn Glu Asp Asp Gly Tyr Asp Val Pro Lys Pro Pro Val Pro Ala Val 770 775 780	2352
ctg gcc cgc cga act ctc tca gat atc tct aat gcc agc tcc tcc ttt Leu Ala Arg Arg Thr Leu Ser Asp Ile Ser Asn Ala Ser Ser Ser Phe 785 790 795 800	2400
ggc tgg ttg tct ctg gat ggt gat cct aca aca aat gtc act gaa ggt Gly Trp Leu Ser Leu Asp Gly Asp Pro Thr Thr Asn Val Thr Glu Gly 805 810 815	2448
tcc caa gtt ccc gag agg cct cca aaa cca ttc ccg cgg aga atc aac Ser Gln Val Pro Glu Arg Pro Pro Lys Pro Phe Pro Arg Arg Ile Asn 820 825 830	2496
tct gaa cgg aaa gct ggc agc tgt cag caa ggt agt ggt cct gcc gcc Ser Glu Arg Lys Ala Gly Ser Cys Gln Gln Gly Ser Gly Pro Ala Ala 835 840 845	2544
tct gct gcc acc gcc tca cct cag ctc tcc agt gag atc gag aac ctc Ser Ala Ala Thr Ala Ser Pro Gln Leu Ser Ser Glu Ile Glu Asn Leu 850 855 860	2592
atg agt cag ggg tac tcc tac cag gac atc cag aaa gct ttg gtc att Met Ser Gln Gly Tyr Ser Tyr Gln Asp Ile Gln Lys Ala Leu Val Ile 865 870 875 880	2640
gcc cag aac aac atc gag atg gcc aaa aac atc ctc ccg gaa ttt gtt Ala Gln Asn Asn Ile Glu Met Ala Lys Asn Ile Leu Arg Glu Phe Val 885 890 895	2688
tcc att tct tct cct gcc cat gta gct acc tag Ser Ile Ser Ser Pro Ala His Val Ala Thr 900 905	2721

<210> 250  
 <211> 906  
 <212> PRT  
 <213> Artificial

<220>

<223> Synthetic Construct

<400> 250

Met Ala Gly Asn Val Lys Lys Ser Ser Gly Ala Gly Gly Gly Thr Gly  
1 5 10 15

Ser Gly Gly Ser Gly Gly Leu Ile Gly Leu Met Lys Asp Ala  
20 25 30

Phe Gln Pro His His His His His His Leu Ser Pro His Pro Pro  
35 40 45

Gly Thr Val Asp Lys Lys Met Val Glu Lys Cys Trp Lys Leu Met Asp  
50 55 60

Lys Val Val Arg Leu Cys Gln Asn Pro Lys Leu Ala Leu Lys Asn Ser  
65 70 75 80

Pro Pro Tyr Ile Leu Asp Leu Leu Pro Asp Thr Tyr Gln His Leu Arg  
85 90 95

Thr Ile Leu Ser Arg Tyr Glu Gly Lys Met Glu Thr Leu Gly Glu Asn  
100 105 110

Glu Tyr Phe Arg Val Phe Met Glu Asn Leu Met Lys Lys Thr Lys Gln  
115 120 125

Thr Ile Ser Leu Phe Lys Glu Gly Lys Glu Arg Met Tyr Glu Glu Asn  
130 135 140

Ser Gln Pro Arg Arg Asn Leu Thr Lys Leu Ser Leu Ile Phe Ser His  
145 150 155 160

Met Leu Ala Glu Leu Lys Gly Ile Phe Pro Ser Gly Leu Phe Gln Gly  
165 170 175

Asp Thr Phe Arg Ile Thr Lys Ala Asp Ala Ala Glu Phe Trp Arg Lys  
180 185 190

Ala Phe Gly Glu Lys Thr Ile Val Pro Trp Lys Ser Phe Arg Gln Ala  
195 200 205

Leu His Glu Val His Pro Ile Ser Ser Gly Leu Glu Ala Met Ala Leu  
210 215 220

Lys Ser Thr Ile Asp Leu Thr Cys Asn Asp Tyr Ile Ser Val Phe Glu  
225 230 235 240

Phe Asp Ile Phe Thr Arg Leu Phe Gln Pro Trp Ser Ser Leu Leu Arg  
245 250 255

Asn Trp Asn Ser Leu Ala Val Thr His Pro Gly Tyr Met Ala Phe Leu  
260 265 270

Thr Tyr Asp Glu Val Lys Ala Arg Leu Gln Lys Phe Ile His Lys Pro  
275 280 285

Gly Ser Tyr Ile Phe Arg Leu Ser Cys Thr Arg Leu Gly Gln Trp Ala  
290 295 300

Ile Glu Tyr Val Thr Ala Asp Gly Asn Ile Leu Gln Thr Ile Pro His  
305 310 315 320

Asn Lys Pro Leu Phe Gln Ala Leu Ile Asp Gly Phe Arg Glu Gly Phe  
325 330 335

Tyr Leu Phe Pro Asp Gly Arg Asn Gln Asn Pro Asp Leu Thr Gly Leu  
340 345 350

Cys Glu Pro Thr Pro Gln Asp His Ile Lys Val Thr Gln Glu Gln Tyr  
355 360 365

Glu Leu Tyr Cys Glu Met Gly Ser Thr Phe Gln Leu Cys Lys Ile Cys  
370 375 380

Ala Glu Asn Asp Lys Asp Val Lys Ile Glu Pro Cys Gly His Leu Met  
385 390 395 400

Cys Thr Ser Cys Leu Thr Ser Trp Gln Glu Ser Gly Gln Gly Cys  
405 410 415

Pro Phe Cys Arg Cys Glu Ile Lys Gly Thr Glu Pro Ile Val Val Asp  
420 425 430

Pro Phe Asp Pro Arg Gly Ser Gly Ser Leu Leu Arg Gln Gly Ala Glu  
435 440 445

Gly Ala Pro Ser Pro Asn Tyr Asp Asp Asp Asp Asp Glu Arg Ala Asp  
450 455 460

Asp Thr Leu Phe Met Met Lys Glu Leu Ala Gly Ala Lys Val Glu Arg  
465 470 475 480

Pro Pro Ser Pro Phe Ser Met Ala Pro Gln Ala Ser Leu Pro Pro Val  
485 490 495

Pro Pro Arg Leu Asp Leu Leu Pro Gln Arg Val Cys Val Pro Ser Ser  
500 505 510

Ala Ser Ala Leu Gly Thr Ala Ser Lys Ala Ala Ser Gly Ser Leu His  
515 520 525

Lys Asp Lys Pro Leu Pro Val Pro Pro Thr Leu Arg Asp Leu Pro Pro  
530 535 540

Pro Pro Pro Pro Asp Arg Pro Tyr Ser Val Gly Ala Glu Ser Arg Pro  
545 550 555 560

Gln Arg Arg Pro Leu Pro Cys Thr Pro Gly Asp Cys Pro Ser Arg Asp  
565 570 575

Lys Leu Pro Pro Val Pro Ser Ser Arg Leu Gly Asp Ser Trp Leu Pro  
580 585 590

Arg Pro Ile Pro Lys Val Pro Val Ser Ala Pro Ser Ser Ser Asp Pro  
595 600 605

Trp Thr Gly Arg Glu Leu Thr Asn Arg His Ser Leu Pro Phe Ser Leu  
610 615 620

Pro Ser Gln Met Glu Pro Arg Pro Asp Val Pro Arg Leu Gly Ser Thr  
625 630 635 640

Phe Ser Leu Asp Thr Ser Met Ser Met Asn Ser Ser Pro Leu Val Gly  
645 650 655

Pro Glu Cys Asp His Pro Lys Ile Lys Pro Ser Ser Ser Ala Asn Ala

660

665

670

Ile Tyr Ser Leu Ala Ala Arg Pro Leu Pro Val Pro Lys Leu Pro Pro  
675 680 685

Gly Glu Gln Cys Glu Gly Glu Asp Thr Glu Tyr Met Thr Pro Ser  
690 695 700

Ser Arg Pro Leu Arg Pro Leu Asp Thr Ser Gln Ser Ser Arg Ala Cys  
705 710 715 720

Asp Cys Asp Gln Gln Ile Asp Ser Cys Thr Tyr Glu Ala Met Tyr Asn  
725 730 735

Ile Gln Ser Gln Ala Pro Ser Ile Thr Glu Ser Ser Thr Phe Gly Glu  
740 745 750

Gly Asn Leu Ala Ala Ala His Ala Asn Thr Gly Pro Glu Glu Ser Glu  
755 760 765

Asn Glu Asp Asp Gly Tyr Asp Val Pro Lys Pro Pro Val Pro Ala Val  
770 775 780

Leu Ala Arg Arg Thr Leu Ser Asp Ile Ser Asn Ala Ser Ser Ser Phe  
785 790 795 800

Gly Trp Leu Ser Leu Asp Gly Asp Pro Thr Thr Asn Val Thr Glu Gly  
805 810 815

Ser Gln Val Pro Glu Arg Pro Pro Lys Pro Phe Pro Arg Arg Ile Asn  
820 825 830

Ser Glu Arg Lys Ala Gly Ser Cys Gln Gln Gly Ser Gly Pro Ala Ala  
835 840 845

Ser Ala Ala Thr Ala Ser Pro Gln Leu Ser Ser Glu Ile Glu Asn Leu  
850 855 860

Met Ser Gln Gly Tyr Ser Tyr Gln Asp Ile Gln Lys Ala Leu Val Ile  
865 870 875 880

Ala Gln Asn Asn Ile Glu Met Ala Lys Asn Ile Leu Arg Glu Phe Val  
885 890 895

Ser Ile Ser Ser Pro Ala His Val Ala Thr  
900 905

<210> 251  
<211> 2721  
<212> DNA  
<213> Artificial

<220>  
<223> c-Cbl C381A

<220>  
<221> CDS  
<222> (1) .. (2718)

<400> 251  
atg gcc ggc aac gtg aag aag agc tct ggg gcc ggg ggc ggc acg ggc 48  
Met Ala Gly Asn Val Lys Lys Ser Ser Gly Ala Gly Gly Gly Thr Gly  
1 5 10 15

tcc ggg ggc tcg ggt tcg ggt ggc ctg att ggg ctc atg aag gac gcc 96  
 Ser Gly Gly Ser Gly Ser Gly Gly Leu Ile Gly Leu Met Lys Asp Ala  
 20 25 30

ttc cag ccg cac cac cac cac cac ctc agc ccc cac ccg ccg 144  
 Phe Gln Pro His His His His His His Leu Ser Pro His Pro Pro  
 35 40 45

ggg acg gtg gac aag aag atg gtg gag aag tgc tgg aag ctc atg gac 192  
 Gly Thr Val Asp Lys Lys Met Val Glu Lys Cys Trp Lys Leu Met Asp  
 50 55 60

aag gtg gtg cgg ttg tgt cag aac cca aag ctg gcg cta aag aat agc	240
Lys Val Val Arg Leu Cys Gln Asn Pro Lys Leu Ala Leu Lys Asn Ser	
65 70 75 80	

cca cct tat atc tta gac ctg cta cca gat acc tac cag cat ctc cgt 288  
 Pro Pro Tyr Ile Leu Asp Leu Leu Pro Asp Thr Tyr Gln His Leu Arg  
 85 90 95

```

act atc ttg tca aga tat gag ggg aag atg gag aca ctt gga gaa aat 336
Thr Ile Leu Ser Arg Tyr Glu Gly Lys Met Glu Thr Leu Gly Glu Asn
100          105          110

```

```

gag tat ttt agg gtg ttt atg gag aat ttg atg aag aaa act aag caa      384
Glu Tyr Phe Arg Val Phe Met Glu Asn Leu Met Lys Lys Thr Lys Gln
.          115           120           125

```

```

acc ata agc ctc ttc aag gag gga aaa gaa aga atg tat gag gag aat 432
Thr Ile Ser Leu Phe Lys Glu Gly Lys Glu Arg Met Tyr Glu Glu Asn
130           135           140

```

tct cag cct agg cga aac cta acc aaa ctg tcc ctc atc ttc agc cac 480

Ser Gln Pro Arg Arg Asn Leu Thr Lys Leu Ser Leu Ile Phe Ser His			
145	150	155	160
atg ctg gca gaa cta aaa gga atc ttt cca agt gga ctc ttt cag gga			528
Met Leu Ala Glu Leu Lys Gly Ile Phe Pro Ser Gly Leu Phe Gln Gly			
165	170	175	
gac aca ttt cgg att act aaa gca gat gct gcg gaa ttt tgg aga aaa			576
Asp Thr Phe Arg Ile Thr Lys Ala Asp Ala Ala Glu Phe Trp Arg Lys			
180	185	190	
gct ttt ggg gaa aag aca ata gtc cct tgg aag agc ttt cga cag gct			624
Ala Phe Gly Glu Lys Thr Ile Val Pro Trp Lys Ser Phe Arg Gln Ala			
195	200	205	
cta cat gaa gtg cat ccc atc agt tct ggg ctg gag gcc atg gct ctg			672
Leu His Glu Val His Pro Ile Ser Ser Gly Leu Glu Ala Met Ala Leu			
210	215	220	
aaa tcc act att gat ctg acc tgc aat gat tat att tcg gtt ttt gaa			720
Lys Ser Thr Ile Asp Leu Thr Cys Asn Asp Tyr Ile Ser Val Phe Glu			
225	230	235	240
ttt gac atc ttt acc cga ctc ttt cag ccc tgg tcc tct ttg ctc agg			768
Phe Asp Ile Phe Thr Arg Leu Phe Gln Pro Trp Ser Ser Leu Leu Arg			
245	250	255	
aat tgg aac agc ctt gct gta act cat cct ggc tac atg gct ttt ttg			816
Asn Trp Asn Ser Leu Ala Val Thr His Pro Gly Tyr Met Ala Phe Leu			
260	265	270	
acg tat gac gaa gtg aaa gct cgg ctc cag aaa ttc att cac aaa cct			864
Thr Tyr Asp Glu Val Lys Ala Arg Leu Gln Lys Phe Ile His Lys Pro			
275	280	285	
ggc agt tat atc ttc cgg ctg agc tgt act cgt ctg ggt cag tgg gct			912
Gly Ser Tyr Ile Phe Arg Leu Ser Cys Thr Arg Leu Gly Gln Trp Ala			
290	295	300	
att ggg tat gtt act gct gat ggg aac att ctc cag aca atc cct cac			960
Ile Gly Tyr Val Thr Ala Asp Gly Asn Ile Leu Gln Thr Ile Pro His			
305	310	315	320
aat aaa cct ctc ttc caa gca ctg att gat ggc ttc agg gaa ggc ttc			1008
Asn Lys Pro Leu Phe Gln Ala Leu Ile Asp Gly Phe Arg Glu Gly Phe			
325	330	335	
tat ttg ttt cct gat gga cga aat cag aat cct gat ctg act ggc tta			1056
Tyr Leu Phe Pro Asp Gly Arg Asn Gln Asn Pro Asp Leu Thr Gly Leu			
340	345	350	
tgt gaa cca act ccc caa gac cat atc aaa gtg acc cag gaa caa tat			1104
Cys Glu Pro Thr Pro Gln Asp His Ile Lys Val Thr Gln Glu Gln Tyr			
355	360	365	
gaa tta tac tgt gag atg ggc tcc aca ttc caa cta gct aaa ata tgt			1152
Glu Leu Tyr Cys Glu Met Gly Ser Thr Phe Gln Leu Ala Lys Ile Cys			

370	375	380	
gct gaa aat gat aag gat gta aag att gag ccc tgt gga cac ctc atg Ala Glu Asn Asp Lys Asp Val Lys Ile Glu Pro Cys Gly His Leu Met 385 390 395 400			1200
tgc aca tcc tgt ctt aca tcc tgg cag gaa tca gaa ggt cag ggc tgt Cys Thr Ser Cys Leu Thr Ser Trp Gln Glu Ser Glu Gly Gln Gly Cys 405 410 415			1248
cct ttc tgc cga tgt gaa att aaa ggt act gaa ccc atc gtg gta gat Pro Phe Cys Arg Cys Glu Ile Lys Gly Thr Glu Pro Ile Val Val Asp 420 425 430			1296
ccg ttt gat cct aga ggg agt ggc agc ctg ttg agg caa gga gca gag Pro Phe Asp Pro Arg Gly Ser Gly Ser Leu Leu Arg Gln Gly Ala Glu 435 440 445			1344
gga gct ccc tcc cca aat tat gat gat gat gat gaa cga gct gat Gly Ala Pro Ser Pro Asn Tyr Asp Asp Asp Asp Glu Arg Ala Asp 450 455 460			1392
gat act ctc ttc atg atg aag gaa ttg gct ggt gcc aag gtg gaa cgg Asp Thr Leu Phe Met Met Lys Glu Leu Ala Gly Ala Lys Val Glu Arg 465 470 475 480			1440
ccg cct tct cca ttc tcc atg gcc cca caa gct tcc ctt ccc ccg gtg Pro Pro Ser Pro Phe Ser Met Ala Pro Gln Ala Ser Leu Pro Pro Val 485 490 495			1488
cca cca cga ctt gac ctt ctg ccg cag cga gta tgt gtt ccc tca agt Pro Pro Arg Leu Asp Leu Leu Pro Gln Arg Val Cys Val Pro Ser Ser 500 505 510			1536
gct tct gct ctt gga act gct tct aag gct gct tct ggc tcc ctt cat Ala Ser Ala Leu Gly Thr Ala Ser Lys Ala Ala Ser Gly Ser Leu His 515 520 525			1584
aaa gac aaa cca ttg cca gta cct ccc aca ctt cga gat ctt cca cca Lys Asp Lys Pro Leu Pro Val Pro Pro Thr Leu Arg Asp Leu Pro Pro 530 535 540			1632
cca ccg cct cca gac cgg cca tat tct gtt gga gca gaa tcc cga cct Pro Pro Pro Pro Asp Arg Pro Tyr Ser Val Gly Ala Glu Ser Arg Pro 545 550 555 560			1680
caa aga cgc ccc ttg cct tgt aca cca ggc gac tgt ccc tcc aga gac Gln Arg Arg Pro Leu Pro Cys Thr Pro Gly Asp Cys Pro Ser Arg Asp 565 570 575			1728
aaa ctg ccc cct gtc ccc tct agc cgc ctt gga gac tca tgg ctg ccc Lys Leu Pro Pro Val Pro Ser Ser Arg Leu Gly Asp Ser Trp Leu Pro 580 585 590			1776
cg <sup>g</sup> cca atc ccc aaa gta cca gta tct gcc cca agt tcc agt gat ccc Arg Pro Ile Pro Lys Val Pro Val Ser Ala Pro Ser Ser Ser Asp Pro 595 600 605			1824

tgg aca gga aga gaa tta acc aac cgg cac tca ctt cca ttt tca ttg Trp Thr Gly Arg Glu Leu Thr Asn Arg His Ser Leu Pro Phe Ser Leu 610 615 620	1872
ccc tca caa atg gag ccc aga cca gat gtg cct agg ctc gga agc acg Pro Ser Gln Met Glu Pro Arg Pro Asp Val Pro Arg Leu Gly Ser Thr 625 630 635 640	1920
ttc agt ctg gat acc tcc atg agt atg aat agc agc cca tta gta ggt Phe Ser Leu Asp Thr Ser Met Ser Met Asn Ser Ser Pro Leu Val Gly 645 650 655	1968
cca gag tgt gac cac ccc aaa atc aaa cct tcc tca tct gcc aat gcc Pro Glu Cys Asp His Pro Lys Ile Lys Pro Ser Ser Ser Ala Asn Ala 660 665 670	2016
att tat tct ctg gct gcc aga cct ctt cct gtg cca aaa ctg cca cct Ile Tyr Ser Leu Ala Ala Arg Pro Leu Pro Val Pro Lys Leu Pro Pro 675 680 685	2064
ggg gag caa tgt gag ggt gaa gag gac aca gag tac atg act ccc tct Gly Glu Gln Cys Glu Gly Glu Asp Thr Glu Tyr Met Thr Pro Ser 690 695 700	2112
tcc agg cct cta cgg cct ttg gat aca tcc cag agt tca cga gca tgt Ser Arg Pro Leu Arg Pro Leu Asp Thr Ser Gln Ser Ser Arg Ala Cys 705 710 715 720	2160
gat tgc gac cag cag att gat agc tgt acg tat gaa gca atg tat aat Asp Cys Asp Gln Gln Ile Asp Ser Cys Thr Tyr Glu Ala Met Tyr Asn 725 730 735	2208
att cag tcc cag gcg cca tct atc acc gag agc agc acc ttt ggt gaa Ile Gln Ser Gln Ala Pro Ser Ile Thr Glu Ser Ser Thr Phe Gly Glu 740 745 750	2256
ggg aat ttg gcc gca gcc cat gcc aac act ggt ccc gag gag tca gaa Gly Asn Leu Ala Ala Ala His Ala Asn Thr Gly Pro Glu Glu Ser Glu 755 760 765	2304
aat gag gat gat ggg tat gat gtc cca aag cca cct gtg ccg gcc gtg Asn Glu Asp Asp Gly Tyr Asp Val Pro Lys Pro Pro Val Pro Ala Val 770 775 780	2352
ctg gcc cgc cga act ctc tca gat atc tct aat gcc agc tcc tcc ttt Leu Ala Arg Arg Thr Leu Ser Asp Ile Ser Asn Ala Ser Ser Ser Phe 785 790 795 800	2400
ggc tgg ttg tct ctg gat ggt gat cct aca aca aat gtc act gaa ggt Gly Trp Leu Ser Leu Asp Gly Asp Pro Thr Thr Asn Val Thr Glu Gly 805 810 815	2448
tcc caa gtt ccc gag agg cct cca aaa cca ttc ccg cg aga atc aac Ser Gln Val Pro Glu Arg Pro Pro Lys Pro Phe Pro Arg Arg Ile Asn 820 825 830	2496

tct gaa cg <sup>g</sup> aaa gct ggc agc t <sup>t</sup> g cag caa ggt agt ggt cct gcc g <sup>c</sup> c	2544
Ser Glu Arg Lys Ala Gly Ser Cys Gln Gln Gly Ser Gly Pro Ala Ala	
835 840 845	
tct gct gcc acc gcc tca cct cag ctc tcc agt gag atc gag aac ctc	2592
Ser Ala Ala Thr Ala Ser Pro Gln Leu Ser Ser Glu Ile Glu Asn Leu	
850 855 860	
atg agt cag ggg tac tcc tac cag gac atc cag aaa gct ttg gtc att	2640
Met Ser Gln Gly Tyr Ser Tyr Gln Asp Ile Gln Lys Ala Leu Val Ile	
865 870 875 880	
gcc cag aac aac atc gag atg gcc aaa aac atc ctc cgg gaa ttt gtt	2688
Ala Gln Asn Asn Ile Glu Met Ala Lys Asn Ile Leu Arg Glu Phe Val	
885 890 895	
tcc att tct tct cct gcc cat gta gct acc tag	2721
Ser Ile Ser Ser Pro Ala His Val Ala Thr	
900 905	

<210> 252  
 <211> 906  
 <212> PRT  
 <213> Artificial

<220>  
 <223> Synthetic Construct

<400> 252

Met Ala Gly Asn Val Lys Lys Ser Ser Gly Ala Gly Gly Gly Thr Gly  
1 5 10 15

Ser Gly Gly Ser Gly Ser Gly Leu Ile Gly Leu Met Lys Asp Ala  
20 25 30

Phe Gln Pro His His His His His His Leu Ser Pro His Pro Pro  
35 40 45

Gly Thr Val Asp Lys Lys Met Val Glu Lys Cys Trp Lys Leu Met Asp  
50 55 60

Lys Val Val Arg Leu Cys Gln Asn Pro Lys Leu Ala Leu Lys Asn Ser  
65 70 75 80

Pro Pro Tyr Ile Leu Asp Leu Leu Pro Asp Thr Tyr Gln His Leu Arg  
85 90 95

Thr Ile Leu Ser Arg Tyr Glu Gly Lys Met Glu Thr Leu Gly Glu Asn  
100 105 110

Glu Tyr Phe Arg Val Phe Met Glu Asn Leu Met Lys Lys Thr Lys Gln  
115 120 125

Thr Ile Ser Leu Phe Lys Glu Gly Lys Glu Arg Met Tyr Glu Glu Asn  
130 135 140

Ser Gln Pro Arg Arg Asn Leu Thr Lys Leu Ser Leu Ile Phe Ser His  
145 150 155 160

Met Leu Ala Glu Leu Lys Gly Ile Phe Pro Ser Gly Leu Phe Gln Gly  
165 170 175

Asp Thr Phe Arg Ile Thr Lys Ala Asp Ala Ala Glu Phe Trp Arg Lys  
180 185 190

Ala Phe Gly Glu Lys Thr Ile Val Pro Trp Lys Ser Phe Arg Gln Ala  
195 200 205

Leu His Glu Val His Pro Ile Ser Ser Gly Leu Glu Ala Met Ala Leu  
210 215 220

Lys Ser Thr Ile Asp Leu Thr Cys Asn Asp Tyr Ile Ser Val Phe Glu  
225 230 235 240

Phe Asp Ile Phe Thr Arg Leu Phe Gln Pro Trp Ser Ser Leu Leu Arg  
245 250 255

Asn Trp Asn Ser Leu Ala Val Thr His Pro Gly Tyr Met Ala Phe Leu  
260 265 270

Thr Tyr Asp Glu Val Lys Ala Arg Leu Gln Lys Phe Ile His Lys Pro  
275 280 285

Gly Ser Tyr Ile Phe Arg Leu Ser Cys Thr Arg Leu Gly Gln Trp Ala  
290 295 300

Ile Gly Tyr Val Thr Ala Asp Gly Asn Ile Leu Gln Thr Ile Pro His  
305 310 315 320

Asn Lys Pro Leu Phe Gln Ala Leu Ile Asp Gly Phe Arg Glu Gly Phe  
325 330 335

Tyr Leu Phe Pro Asp Gly Arg Asn Gln Asn Pro Asp Leu Thr Gly Leu  
340 345 350

Cys Glu Pro Thr Pro Gln Asp His Ile Lys Val Thr Gln Glu Gln Tyr  
355 360 365

Glu Leu Tyr Cys Glu Met Gly Ser Thr Phe Gln Leu Ala Lys Ile Cys  
370 375 380

Ala Glu Asn Asp Lys Asp Val Lys Ile Glu Pro Cys Gly His Leu Met  
385 390 395 400

Cys Thr Ser Cys Leu Thr Ser Trp Gln Glu Ser Glu Gly Gln Gly Cys  
405 410 415

Pro Phe Cys Arg Cys Glu Ile Lys Gly Thr Glu Pro Ile Val Val Asp  
420 425 430

Pro Phe Asp Pro Arg Gly Ser Gly Ser Leu Leu Arg Gln Gly Ala Glu  
435 440 445

Gly Ala Pro Ser Pro Asn Tyr Asp Asp Asp Asp Glu Arg Ala Asp  
450 455 460

Asp Thr Leu Phe Met Met Lys Glu Leu Ala Gly Ala Lys Val Glu Arg  
465 470 475 480

Pro Pro Ser Pro Phe Ser Met Ala Pro Gln Ala Ser Leu Pro Pro Val  
485 490 495

Pro Pro Arg Leu Asp Leu Leu Pro Gln Arg Val Cys Val Pro Ser Ser  
500 505 510

Ala Ser Ala Leu Gly Thr Ala Ser Lys Ala Ala Ser Gly Ser Leu His  
515 520 525

Lys Asp Lys Pro Leu Pro Val Pro Pro Thr Leu Arg Asp Leu Pro Pro  
530 535 540

Pro Pro Pro Pro Asp Arg Pro Tyr Ser Val Gly Ala Glu Ser Arg Pro  
545 550 555 560

Gln Arg Arg Pro Leu Pro Cys Thr Pro Gly Asp Cys Pro Ser Arg Asp  
565 570 575

Lys Leu Pro Pro Val Pro Ser Ser Arg Leu Gly Asp Ser Trp Leu Pro  
580 585 590

Arg Pro Ile Pro Lys Val Pro Val Ser Ala Pro Ser Ser Asp Pro  
595 600 605

Trp Thr Gly Arg Glu Leu Thr Asn Arg His Ser Leu Pro Phe Ser Leu  
610 615 620

Pro Ser Gln Met Glu Pro Arg Pro Asp Val Pro Arg Leu Gly Ser Thr  
625 630 635 640

Phe Ser Leu Asp Thr Ser Met Ser Met Asn Ser Ser Pro Leu Val Gly  
645 650 655

Pro Glu Cys Asp His Pro Lys Ile Lys Pro Ser Ser Ala Asn Ala  
660 665 670

Ile Tyr Ser Leu Ala Ala Arg Pro Leu Pro Val Pro Lys Leu Pro Pro  
675 680 685

Gly Glu Gln Cys Glu Gly Glu Asp Thr Glu Tyr Met Thr Pro Ser  
690 695 700

Ser Arg Pro Leu Arg Pro Leu Asp Thr Ser Gln Ser Ser Arg Ala Cys  
705 710 715 720

Asp Cys Asp Gln Gln Ile Asp Ser Cys Thr Tyr Glu Ala Met Tyr Asn  
725 730 735

Ile Gln Ser Gln Ala Pro Ser Ile Thr Glu Ser Ser Thr Phe Gly Glu  
740 745 750

Gly Asn Leu Ala Ala Ala His Ala Asn Thr Gly Pro Glu Glu Ser Glu  
755 760 765

Asn Glu Asp Asp Gly Tyr Asp Val Pro Lys Pro Pro Val Pro Ala Val  
770 775 780

Leu Ala Arg Arg Thr Leu Ser Asp Ile Ser Asn Ala Ser Ser Ser Phe

785

790

795

800

Gly Trp Leu Ser Leu Asp Gly Asp Pro Thr Thr Asn Val Thr Glu Gly  
 805 810 815

Ser Gln Val Pro Glu Arg Pro Pro Lys Pro Phe Pro Arg Arg Ile Asn  
 820 825 830

Ser Glu Arg Lys Ala Gly Ser Cys Gln Gln Gly Ser Gly Pro Ala Ala  
 835 840 845

Ser Ala Ala Thr Ala Ser Pro Gln Leu Ser Ser Glu Ile Glu Asn Leu  
 850 855 860

Met Ser Gln Gly Tyr Ser Tyr Gln Asp Ile Gln Lys Ala Leu Val Ile  
 865 870 875 880

Ala Gln Asn Asn Ile Glu Met Ala Lys Asn Ile Leu Arg Glu Phe Val  
 885 890 895

Ser Ile Ser Ser Pro Ala His Val Ala Thr  
 900 905

&lt;210&gt; 253

&lt;211&gt; 2721

&lt;212&gt; DNA

&lt;213&gt; Artificial

&lt;220&gt;

&lt;223&gt; c-Cbl Y700F

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)..(2718)

&lt;400&gt; 253

atg gcc ggc aac gtg aag aag agc tct ggg gcc ggg ggc ggc acg ggc  
 Met Ala Gly Asn Val Lys Lys Ser Ser Gly Ala Gly Gly Gly Thr Gly  
 1 5 10 15

48

tcc ggg ggc tcg ggt tcg ggt ggc ctg att ggg ctc atg aag gac gcc  
 Ser Gly Gly Ser Gly Ser Gly Gly Leu Ile Gly Leu Met Lys Asp Ala  
 20 25 30

96

ttc cag ccg cac cac cac cac cac ctc agc ccc cac ccg ccg  
 Phe Gln Pro His His His His His His Leu Ser Pro His Pro Pro  
 35 40 45

144

ggg acg gtg gac aag aag atg gtg gag aag tgc tgg aag ctc atg gac Gly Thr Val Asp Lys Lys Met Val Glu Lys Cys Trp Lys Leu Met Asp	50	55	60	192	
aag gtg gtg cgg ttg tgt cag aac cca aag ctg gcg cta aag aat agc Lys Val Val Arg Leu Cys Gln Asn Pro Lys Leu Ala Leu Lys Asn Ser	65	70	75	80	240
cca cct tat atc tta gac ctg cta cca gat acc tac cag cat ctc cgt Pro Pro Tyr Ile Leu Asp Leu Leu Pro Asp Thr Tyr Gln His Leu Arg	85	90	95	288	
act atc ttg tca aga tat gag ggg aag atg gag aca ctt gga gaa aat Thr Ile Leu Ser Arg Tyr Glu Gly Lys Met Glu Thr Leu Gly Glu Asn	100	105	110	336	
gag tat ttt agg gtg ttt atg gag aat ttg atg aag aaa act aag caa Glu Tyr Phe Arg Val Phe Met Glu Asn Leu Met Lys Lys Thr Lys Gln	115	120	125	384	
acc ata agc ctc ttc aag gag gga aaa gaa aga atg tat gag gag aat Thr Ile Ser Leu Phe Lys Glu Gly Lys Glu Arg Met Tyr Glu Glu Asn	130	135	140	432	
tct cag cct agg cga aac cta acc aaa ctg tcc ctc atc ttc agc cac Ser Gln Pro Arg Arg Asn Leu Thr Lys Leu Ser Leu Ile Phe Ser His	145	150	155	160	480
atg ctg gca gaa cta aaa gga atc ttt cca agt gga ctc ttt cag gga Met Leu Ala Glu Leu Lys Gly Ile Phe Pro Ser Gly Leu Phe Gln Gly	165	170	175	528	
gac aca ttt cgg att act aaa gca gat gct gcg gaa ttt tgg aga aaa Asp Thr Phe Arg Ile Thr Lys Ala Asp Ala Ala Glu Phe Trp Arg Lys	180	185	190	576	
gct ttt ggg gaa aag aca ata gtc cct tgg aag agc ttt cga cag gct Ala Phe Gly Glu Lys Thr Ile Val Pro Trp Lys Ser Phe Arg Gln Ala	195	200	205	624	
cta cat gaa gtg cat ccc atc agt tct ggg ctg gag gcc atg gct ctg Leu His Glu Val His Pro Ile Ser Ser Gly Leu Glu Ala Met Ala Leu	210	215	220	672	
aaa tcc act att gat ctg acc tgc aat gat tat att tcg gtt ttt gaa Lys Ser Thr Ile Asp Leu Thr Cys Asn Asp Tyr Ile Ser Val Phe Glu	225	230	235	240	720
ttt gac atc ttt acc cga ctc ttt cag ccc tgg tcc tct ttg ctc agg Phe Asp Ile Phe Thr Arg Leu Phe Gln Pro Trp Ser Ser Leu Leu Arg	245	250	255	768	
aat tgg aac agc ctt gct gta act cat cct ggc tac atg gct ttt ttg Asn Trp Asn Ser Leu Ala Val Thr His Pro Gly Tyr Met Ala Phe Leu	260	265	270	816	
acg tat gac gaa gtg aaa gct cgg ctc cag aaa ttc att cac aaa cct				864	

Thr Tyr Asp Glu Val Lys Ala Arg Leu Gln Lys Phe Ile His Lys Pro			
275	280	285	
ggc agt tat atc ttc cg <sup>g</sup> ctg agc tgt act cgt ctg ggt cag tgg gct			912
Gly Ser Tyr Ile Phe Arg Leu Ser Cys Thr Arg Leu Gly Gln Trp Ala			
290	295	300	
att ggg tat gtt act gct gat ggg aac att ctc cag aca atc cct cac			960
Ile Gly Tyr Val Thr Ala Asp Gly Asn Ile Leu Gln Thr Ile Pro His			
305	310	315	320
aat aaa cct ctc ttc caa gca ctg att gat ggc ttc agg gaa ggc ttc			1008
Asn Lys Pro Leu Phe Gln Ala Leu Ile Asp Gly Phe Arg Glu Gly Phe			
325	330	335	
tat ttg ttt cct gat gga cga aat cag aat cct gat ctg act ggc tta			1056
Tyr Leu Phe Pro Asp Gly Arg Asn Gln Asn Pro Asp Leu Thr Gly Leu			
340	345	350	
tgt gaa cca act ccc caa gac cat atc aaa gtg acc cag gaa caa tat			1104
Cys Glu Pro Thr Pro Gln Asp His Ile Lys Val Thr Gln Glu Gln Tyr			
355	360	365	
gaa tta tac tgt gag atg ggc tcc aca ttc caa cta tgt aaa ata tgt			1152
Glu Leu Tyr Cys Glu Met Gly Ser Thr Phe Gln Leu Cys Lys Ile Cys			
370	375	380	
gct gaa aat gat aag gat gta aag att gag ccc tgt gga cac ctc atg			1200
Ala Glu Asn Asp Lys Asp Val Lys Ile Glu Pro Cys Gly His Leu Met			
385	390	395	400
tgc aca tcc tgt ctt aca tcc tgg cag gaa tca gaa ggt cag ggc tgt			1248
Cys Thr Ser Cys Leu Thr Ser Trp Gln Glu Ser Glu Gly Gln Gly Cys			
405	410	415	
cct ttc tgc cga tgt gaa att aaa ggt act gaa ccc atc gtg gta gat			1296
Pro Phe Cys Arg Cys Glu Ile Lys Gly Thr Glu Pro Ile Val Val Asp			
420	425	430	
ccg ttt gat cct aga ggg agt ggc agc ctg ttg agg caa gga gca gag			1344
Pro Phe Asp Pro Arg Gly Ser Gly Ser Leu Leu Arg Gln Gly Ala Glu			
435	440	445	
gga gct ccc tcc cca aat tat gat gat gat gat gaa cga gct gat			1392
Gly Ala Pro Ser Pro Asn Tyr Asp Asp Asp Asp Glu Arg Ala Asp			
450	455	460	
gat act ctc ttc atg atg aag gaa ttg gct ggt gcc aag gtg gaa cgg			1440
Asp Thr Leu Phe Met Met Lys Glu Leu Ala Gly Ala Lys Val Glu Arg			
465	470	475	480
ccg cct tct cca ttc tcc atg gcc cca caa gct tcc ctt ccc ccg gtg			1488
Pro Pro Ser Pro Phe Ser Met Ala Pro Gln Ala Ser Leu Pro Pro Val			
485	490	495	
cca cca cga ctt gac ctt ctg ccg cag cga gta tgt gtt ccc tca agt			1536
Pro Pro Arg Leu Asp Leu Leu Pro Gln Arg Val Cys Val Pro Ser Ser			

500	505	510	
gct tct gct ctt gga act gct tct aag gct gct tct ggc tcc ctt cat Ala Ser Ala Leu Gly Thr Ala Ser Lys Ala Ala Ser Gly Ser Leu His 515	520	525	1584
aaa gac aaa cca ttg cca gta cct ccc aca ctt cga gat ctt cca cca Lys Asp Lys Pro Leu Pro Val Pro Pro Thr Leu Arg Asp Leu Pro Pro 530	535	540	1632
cca ccg cct cca gac cgg cca tat tct gtt gga gca gaa tcc cga cct Pro Pro Pro Pro Asp Arg Pro Tyr Ser Val Gly Ala Glu Ser Arg Pro 545	550	555	1680
caa aga cgc ccc ttg cct tgt aca cca ggc gac tgt ccc tcc aga gac Gln Arg Arg Pro Leu Pro Cys Thr Pro Gly Asp Cys Pro Ser Arg Asp 565	570	575	1728
aaa ctg ccc cct gtc ccc tct agc cgc ctt gga gac tca tgg ctg ccc Lys Leu Pro Pro Val Pro Ser Ser Arg Leu Gly Asp Ser Trp Leu Pro 580	585	590	1776
cgg cca atc ccc aaa gta cca gta tct gcc cca agt tcc agt gat ccc Arg Pro Ile Pro Lys Val Pro Val Ser Ala Pro Ser Ser Ser Asp Pro 595	600	605	1824
tgg aca gga aga gaa tta acc aac cgg cac tca ctt cca ttt tca ttg Trp Thr Gly Arg Glu Leu Thr Asn Arg His Ser Leu Pro Phe Ser Leu 610	615	620	1872
ccc tca caa atg gag ccc aga cca gat gtg cct agg ctc gga agc acg Pro Ser Gln Met Glu Pro Arg Pro Asp Val Pro Arg Leu Gly Ser Thr 625	630	635	1920
ttc agt ctg gat acc tcc atg agt atg aat agc agc cca tta gta ggt Phe Ser Leu Asp Thr Ser Met Ser Met Asn Ser Ser Pro Leu Val Gly 645	650	655	1968
cca gag tgt gac cac ccc aaa atc aaa cct tcc tca tct gcc aat gcc Pro Glu Cys Asp His Pro Lys Ile Lys Pro Ser Ser Ser Ala Asn Ala 660	665	670	2016
att tat tct ctg gct gcc aga cct ctt cct gtg cca aaa ctg cca cct Ile Tyr Ser Leu Ala Ala Arg Pro Leu Pro Val Pro Lys Leu Pro Pro 675	680	685	2064
ggg gag caa tgt gag ggt gaa gag gac aca gag ttc atg act ccc tct Gly Glu Gln Cys Glu Gly Glu Glu Asp Thr Glu Phe Met Thr Pro Ser 690	695	700	2112
tcc agg cct cta cgg cct ttg gat aca tcc cag agt tca cga gca tgt Ser Arg Pro Leu Arg Pro Leu Asp Thr Ser Gln Ser Ser Arg Ala Cys 705	710	715	2160
gat tgc gac cag cag att gat agc tgt acg tat gaa gca atg tat aat Asp Cys Asp Gln Gln Ile Asp Ser Cys Thr Tyr Glu Ala Met Tyr Asn 725	730	735	2208

att cag tcc cag gcg cca tct atc acc gag agc agc acc ttt ggt gaa Ile Gln Ser Gln Ala Pro Ser Ile Thr Glu Ser Ser Thr Phe Gly Glu 740 745 750	2256
ggg aat ttg gcc gca gcc cat gcc aac act ggt ccc gag gag tca gaa Gly Asn Leu Ala Ala Ala His Ala Asn Thr Gly Pro Glu Glu Ser Glu 755 760 765	2304
aat gag gat gat ggg tat gat gtc cca aag cca cct gtg ccg gcc gtg Asn Glu Asp Asp Gly Tyr Asp Val Pro Lys Pro Pro Val Pro Ala Val 770 775 780	2352
ctg gcc cgc cga act ctc tca gat atc tct aat gcc agc tcc tcc ttt Leu Ala Arg Arg Thr Leu Ser Asp Ile Ser Asn Ala Ser Ser Ser Phe 785 790 795 800	2400
ggc tgg ttg tct ctg gat ggt gat cct aca aca aat gtc act gaa ggt Gly Trp Leu Ser Leu Asp Gly Asp Pro Thr Thr Asn Val Thr Glu Gly 805 810 815	2448
tcc caa gtt ccc gag agg cct cca aaa cca ttc ccg ccg aga atc aac Ser Gln Val Pro Glu Arg Pro Pro Lys Pro Phe Pro Arg Arg Ile Asn 820 825 830	2496
tct gaa cgg aaa gct ggc agc tgt cag caa ggt agt ggt cct gcc gcc Ser Glu Arg Lys Ala Gly Ser Cys Gln Gln Gly Ser Gly Pro Ala Ala 835 840 845	2544
tct gct gcc acc gcc tca cct cag ctc tcc agt gag atc gag aac ctc Ser Ala Ala Thr Ala Ser Pro Gln Leu Ser Ser Glu Ile Glu Asn Leu 850 855 860	2592
atg agt cag ggg tac tcc tac cag gac atc cag aaa gct ttg gtc att Met Ser Gln Gly Tyr Ser Tyr Gln Asp Ile Gln Lys Ala Leu Val Ile 865 870 875 880	2640
gcc cag aac aac atc gag atg gcc aaa aac atc ctc ccg gaa ttt gtt Ala Gln Asn Asn Ile Glu Met Ala Lys Asn Ile Leu Arg Glu Phe Val 885 890 895	2688
tcc att tct tct cct gcc cat gta gct acc tag Ser Ile Ser Ser Pro Ala His Val Ala Thr 900 905	2721

<210> 254  
<211> 906  
<212> PRT  
<213> Artificial

<220>  
<223> Synthetic Construct

<400> 254

Met Ala Gly Asn Val Lys Lys Ser Ser Gly Ala Gly Gly Gly Thr Gly

1

5

10

15

Ser Gly Gly Ser Gly Gly Leu Ile Gly Leu Met Lys Asp Ala  
20 25 30

Phe Gln Pro His His His His His His His Leu Ser Pro His Pro Pro  
35 40 45

Gly Thr Val Asp Lys Lys Met Val Glu Lys Cys Trp Lys Leu Met Asp  
50 55 60

Lys Val Val Arg Leu Cys Gln Asn Pro Lys Leu Ala Leu Lys Asn Ser  
65 70 75 80

Pro Pro Tyr Ile Leu Asp Leu Leu Pro Asp Thr Tyr Gln His Leu Arg  
85 90 95

Thr Ile Leu Ser Arg Tyr Glu Gly Lys Met Glu Thr Leu Gly Glu Asn  
100 105 110

Glu Tyr Phe Arg Val Phe Met Glu Asn Leu Met Lys Lys Thr Lys Gln  
115 120 125

Thr Ile Ser Leu Phe Lys Glu Gly Lys Glu Arg Met Tyr Glu Glu Asn  
130 135 140

Ser Gln Pro Arg Arg Asn Leu Thr Lys Leu Ser Leu Ile Phe Ser His  
145 150 155 160

Met Leu Ala Glu Leu Lys Gly Ile Phe Pro Ser Gly Leu Phe Gln Gly  
165 170 175

Asp Thr Phe Arg Ile Thr Lys Ala Asp Ala Ala Glu Phe Trp Arg Lys  
180 185 190

Ala Phe Gly Glu Lys Thr Ile Val Pro Trp Lys Ser Phe Arg Gln Ala  
195 200 205

Leu His Glu Val His Pro Ile Ser Ser Gly Leu Glu Ala Met Ala Leu  
210 215 220

Lys Ser Thr Ile Asp Leu Thr Cys Asn Asp Tyr Ile Ser Val Phe Glu  
225 230 235 240

Phe Asp Ile Phe Thr Arg Leu Phe Gln Pro Trp Ser Ser Leu Leu Arg  
245 250 255

Asn Trp Asn Ser Leu Ala Val Thr His Pro Gly Tyr Met Ala Phe Leu  
260 265 270

Thr Tyr Asp Glu Val Lys Ala Arg Leu Gln Lys Phe Ile His Lys Pro  
275 280 285

Gly Ser Tyr Ile Phe Arg Leu Ser Cys Thr Arg Leu Gly Gln Trp Ala  
290 295 300

Ile Gly Tyr Val Thr Ala Asp Gly Asn Ile Leu Gln Thr Ile Pro His  
305 310 315 320

Asn Lys Pro Leu Phe Gln Ala Leu Ile Asp Gly Phe Arg Glu Gly Phe  
325 330 335

Tyr Leu Phe Pro Asp Gly Arg Asn Gln Asn Pro Asp Leu Thr Gly Leu  
340 345 350

Cys Glu Pro Thr Pro Gln Asp His Ile Lys Val Thr Gln Glu Gln Tyr  
355 360 365

Glu Leu Tyr Cys Glu Met Gly Ser Thr Phe Gln Leu Cys Lys Ile Cys  
370 375 380

Ala Glu Asn Asp Lys Asp Val Lys Ile Glu Pro Cys Gly His Leu Met  
385 390 395 400

Cys Thr Ser Cys Leu Thr Ser Trp Gln Glu Ser Gly Gln Gly Cys  
405 410 415

Pro Phe Cys Arg Cys Glu Ile Lys Gly Thr Glu Pro Ile Val Val Asp  
420 425 430

Pro Phe Asp Pro Arg Gly Ser Gly Ser Leu Leu Arg Gln Gly Ala Glu  
435 440 445

Gly Ala Pro Ser Pro Asn Tyr Asp Asp Asp Asp Glu Arg Ala Asp  
450 455 460

Asp Thr Leu Phe Met Met Lys Glu Leu Ala Gly Ala Lys Val Glu Arg  
465 470 475 480

Pro Pro Ser Pro Phe Ser Met Ala Pro Gln Ala Ser Leu Pro Pro Val  
485 490 495

Pro Pro Arg Leu Asp Leu Leu Pro Gln Arg Val Cys Val Pro Ser Ser  
500 505 510

Ala Ser Ala Leu Gly Thr Ala Ser Lys Ala Ala Ser Gly Ser Leu His  
515 520 525

Lys Asp Lys Pro Leu Pro Val Pro Pro Thr Leu Arg Asp Leu Pro Pro  
530 535 540

Pro Pro Pro Pro Asp Arg Pro Tyr Ser Val Gly Ala Glu Ser Arg Pro  
545 550 555 560

Gln Arg Arg Pro Leu Pro Cys Thr Pro Gly Asp Cys Pro Ser Arg Asp  
565 570 575

Lys Leu Pro Pro Val Pro Ser Ser Arg Leu Gly Asp Ser Trp Leu Pro  
580 585 590

Arg Pro Ile Pro Lys Val Pro Val Ser Ala Pro Ser Ser Ser Asp Pro  
595 600 605

Trp Thr Gly Arg Glu Leu Thr Asn Arg His Ser Leu Pro Phe Ser Leu  
610 615 620

Pro Ser Gln Met Glu Pro Arg Pro Asp Val Pro Arg Leu Gly Ser Thr  
625 630 635 640

Phe Ser Leu Asp Thr Ser Met Ser Met Asn Ser Ser Pro Leu Val Gly  
645 650 655

Pro Glu Cys Asp His Pro Lys Ile Lys Pro Ser Ser Ser Ala Asn Ala  
660 665 670

Ile Tyr Ser Leu Ala Ala Arg Pro Leu Pro Val Pro Lys Leu Pro Pro  
675 680 685

Gly Glu Gln Cys Glu Gly Glu Glu Asp Thr Glu Phe Met Thr Pro Ser  
690 695 700

Ser Arg Pro Leu Arg Pro Leu Asp Thr Ser Gln Ser Ser Arg Ala Cys  
705 710 715 720

Asp Cys Asp Gln Gln Ile Asp Ser Cys Thr Tyr Glu Ala Met Tyr Asn  
725 730 735

Ile Gln Ser Gln Ala Pro Ser Ile Thr Glu Ser Ser Thr Phe Gly Glu  
740 745 750

Gly Asn Leu Ala Ala Ala His Ala Asn Thr Gly Pro Glu Glu Ser Glu  
755 760 765

Asn Glu Asp Asp Gly Tyr Asp Val Pro Lys Pro Pro Val Pro Ala Val  
770 775 780

Leu Ala Arg Arg Thr Leu Ser Asp Ile Ser Asn Ala Ser Ser Ser Phe  
785 790 795 800

Gly Trp Leu Ser Leu Asp Gly Asp Pro Thr Thr Asn Val Thr Glu Gly  
805 810 815

Ser Gln Val Pro Glu Arg Pro Pro Lys Pro Phe Pro Arg Arg Ile Asn  
820 825 830

Ser Glu Arg Lys Ala Gly Ser Cys Gln Gln Gly Ser Gly Pro Ala Ala  
835 840 845

Ser Ala Ala Thr Ala Ser Pro Gln Leu Ser Ser Glu Ile Glu Asn Leu  
850 855 860

Met Ser Gln Gly Tyr Ser Tyr Gln Asp Ile Gln Lys Ala Leu Val Ile  
865 870 875 880

Ala Gln Asn Asn Ile Glu Met Ala Lys Asn Ile Leu Arg Glu Phe Val  
885 890 895

Ser Ile Ser Ser Pro Ala His Val Ala Thr  
900 905

<211> 2721  
<212> DNA  
<213> Artificial

<220>  
<223> c-Cbl Y731F

<220>  
<221> CDS  
<222> (1) .. (2718)

<400> 255				48
atg gcc ggc aac gtg aag aag agc tct ggg gcc ggg ggc ggc acg ggc	Met Ala Gly Asn Val Lys Lys Ser Ser Gly Ala Gly Gly Gly Thr Gly			
1 5 10 15				
tcc ggg ggc tcg ggt tcg ggt ggc ctg att ggg ctc atg aag gac gcc	Ser Gly Gly Ser Gly Ser Gly Gly Leu Ile Gly Leu Met Lys Asp Ala			96
20 25 30				
ttc cag ccg cac cac cac cac cac ctc agc ccc cac ccg ccg	Phe Gln Pro His His His His His His Leu Ser Pro His Pro Pro			144
35 40 45				
ggg acg gtg gac aag aag atg gtg gag aag tgc tgg aag ctc atg gac	Gly Thr Val Asp Lys Lys Met Val Glu Lys Cys Trp Lys Leu Met Asp			192
50 55 60				
aag gtg gtg cgg ttg tgt cag aac cca aag ctg gcg cta aag aat agc	Lys Val Val Arg Leu Cys Gln Asn Pro Lys Leu Ala Leu Lys Asn Ser			240
65 70 75 80				
cca cct tat atc tta gac ctg cta cca gat acc tac cag cat ctc cgt	Pro Pro Tyr Ile Leu Asp Leu Leu Pro Asp Thr Tyr Gln His Leu Arg			288
85 90 95				
act atc ttg tca aga tat gag ggg aag atg gag aca ctt gga gaa aat	Thr Ile Leu Ser Arg Tyr Glu Gly Lys Met Glu Thr Leu Gly Glu Asn			336
100 105 110				
gag tat ttt agg gtg ttt atg gag aat ttg atg aag aaa act aag caa	Glu Tyr Phe Arg Val Phe Met Glu Asn Leu Met Lys Lys Thr Lys Gln			384
115 120 125				
acc ata agc ctc ttc aag gag gga aaa gaa aga atg tat gag gag aat	Thr Ile Ser Leu Phe Lys Glu Gly Lys Glu Arg Met Tyr Glu Glu Asn			432
130 135 140				
tct cag cct agg cga aac cta acc aaa ctg tcc ctc atc ttc agc cac	Ser Gln Pro Arg Arg Asn Leu Thr Lys Leu Ser Leu Ile Phe Ser His			480
145 150 155 160				
atg ctg gca gaa cta aaa gga atc ttt cca agt gga ctc ttt cag gga	Met Leu Ala Glu Leu Lys Gly Ile Phe Pro Ser Gly Leu Phe Gln Gly			528
165 170 175				

gac aca ttt cg <sup>g</sup> att act aaa gca gat gct g <sup>c</sup> gaa ttt tgg aga aaa Asp Thr Phe Arg Ile Thr Lys Ala Asp Ala Ala Glu Phe Trp Arg Lys 180 185 190	576
gct ttt ggg gaa aag aca ata gtc cct tgg aag agc ttt cga cag gct Ala Phe Gly Glu Lys Thr Ile Val Pro Trp Lys Ser Phe Arg Gln Ala 195 200 205	624
cta cat gaa gtg cat ccc atc agt tct ggg ctg gag gcc atg gct ctg Leu His Glu Val His Pro Ile Ser Ser Gly Leu Glu Ala Met Ala Leu 210 215 220	672
aaa tcc act att gat ctg acc tgc aat gat tat att tcg gtt ttt gaa Lys Ser Thr Ile Asp Leu Thr Cys Asn Asp Tyr Ile Ser Val Phe Glu 225 230 235 240	720
ttt gac atc ttt acc cga ctc ttt cag ccc tgg tcc tct ttg ctc agg Phe Asp Ile Phe Thr Arg Leu Phe Gln Pro Trp Ser Ser Leu Leu Arg 245 250 255	768
aat tgg aac agc ctt gct gta act cat cct ggc tac atg gct ttt ttg Asn Trp Asn Ser Leu Ala Val Thr His Pro Gly Tyr Met Ala Phe Leu 260 265 270	816
acg tat gac gaa gtg aaa gct cgg ctc cag aaa ttc att cac aaa cct Thr Tyr Asp Glu Val Lys Ala Arg Leu Gln Lys Phe Ile His Lys Pro 275 280 285	864
ggc agt tat atc ttc cgg ctg agc tgt act cgt ctg ggt cag tgg gct Gly Ser Tyr Ile Phe Arg Leu Ser Cys Thr Arg Leu Gly Gln Trp Ala 290 295 300	912
att ggg tat gtt act gct gat ggg aac att ctc cag aca atc cct cac Ile Gly Tyr Val Thr Ala Asp Gly Asn Ile Leu Gln Thr Ile Pro His 305 310 315 320	960
aat aaa cct ctc ttc caa gca ctg att gat ggc ttc agg gaa g <sup>g</sup> c ttc Asn Lys Pro Leu Phe Gln Ala Leu Ile Asp Gly Phe Arg Glu Gly Phe 325 330 335	1008
tat ttg ttt cct gat gga cga aat cag aat cct gat ctg act ggc tta Tyr Leu Phe Pro Asp Gly Arg Asn Gln Asn Pro Asp Leu Thr Gly Leu 340 345 350	1056
tgt gaa cca act ccc caa gac cat atc aaa gtg acc cag gaa caa tat Cys Glu Pro Thr Pro Gln Asp His Ile Lys Val Thr Gln Glu Gln Tyr 355 360 365	1104
gaa tta tac tgt gag atg ggc tcc aca ttc caa cta tgt aaa ata tgt Glu Leu Tyr Cys Glu Met Gly Ser Thr Phe Gln Leu Cys Lys Ile Cys 370 375 380	1152
gct gaa aat gat aag gat gta aag att gag ccc tgt gga cac ctc atg Ala Glu Asn Asp Lys Asp Val Lys Ile Glu Pro Cys Gly His Leu Met 385 390 395 400	1200
tgc aca tcc tgt ctt aca tcc tgg cag gaa tca gaa ggt cag ggc tgt	1248

Cys	Thr	Ser	Cys	Leu	Thr	Ser	Trp	Gln	Glu	Ser	Glu	Gly	Gln	Gly	Cys	
				405				410						415		
cct	ttc	tgc	cga	tgt	gaa	att	aaa	ggt	act	gaa	ccc	atc	gtg	gta	gat	1296
Pro	Phe	Cys	Arg	Cys	Glu	Ile	Lys	Gly	Thr	Glu	Pro	Ile	Val	Val	Asp	
	420				425				430							
ccg	ttt	gat	cct	aga	ggg	agt	ggc	agc	ctg	ttg	agg	caa	gga	gca	gag	1344
Pro	Phe	Asp	Pro	Arg	Gly	Ser	Gly	Ser	Leu	Leu	Arg	Gln	Gly	Ala	Glu	
	435			440					445							
gga	gct	ccc	tcc	cca	aat	tat	gat	gat	gat	gat	gaa	cga	gct	gat		1392
Gly	Ala	Pro	Ser	Pro	Asn	Tyr	Asp	Asp	Asp	Asp	Asp	Glu	Arg	Ala	Asp	
	450			455			460									
gat	act	ctc	ttc	atg	atg	aag	gaa	ttg	gct	ggt	gcc	aag	gtg	gaa	cg	1440
Asp	Thr	Leu	Phe	Met	Met	Lys	Glu	Leu	Ala	Gly	Ala	Lys	Val	Glu	Arg	
	465			470			475		480							
ccg	cct	tct	cca	tcc	tcc	atg	gcc	cca	caa	gct	tcc	ctt	ccc	ccg	gt	1488
Pro	Pro	Ser	Pro	Phe	Ser	Met	Ala	Pro	Gln	Ala	Ser	Leu	Pro	Pro	Val	
	485					490			495							
cca	cca	cga	ctt	gac	ctt	ctg	ccg	cag	cga	gta	tgt	gtt	ccc	tca	agt	1536
Pro	Pro	Arg	Leu	Asp	Leu	Leu	Pro	Gln	Arg	Val	Cys	Val	Pro	Ser	Ser	
	500				505				510							
gct	tct	ctt	gga	act	gct	tct	aag	gct	gct	tct	ggc	tcc	ctt	cat		1584
Ala	Ser	Ala	Leu	Gly	Thr	Ala	Ser	Lys	Ala	Ala	Ser	Gly	Ser	Leu	His	
	515			520			525									
aaa	gac	aaa	cca	ttg	cca	gta	cct	ccc	aca	ctt	cga	gat	ctt	cca	cca	1632
Lys	Asp	Lys	Pro	Leu	Pro	Val	Pro	Pro	Thr	Leu	Arg	Asp	Leu	Pro	Pro	
	530				535				540							
cca	ccg	cct	cca	gac	cg	cca	tat	tct	gtt	gga	gca	gaa	tcc	cga	cct	1680
Pro	Pro	Pro	Asp	Arg	Pro	Tyr	Ser	Val	Gly	Ala	Glu	Ser	Arg	Pro		
	545			550			555		560							
caa	aga	cgc	ccc	ttg	cct	tgt	aca	cca	ggc	gac	tgt	ccc	tcc	aga	gac	1728
Gln	Arg	Arg	Pro	Leu	Pro	Cys	Thr	Pro	Gly	Asp	Cys	Pro	Ser	Arg	Asp	
	565				570			575								
aaa	ctg	ccc	cct	gtc	ccc	tct	agc	cgc	ctt	gga	gac	tca	tgg	ctg	ccc	1776
Lys	Leu	Pro	Pro	Val	Pro	Ser	Ser	Arg	Leu	Gly	Asp	Ser	Trp	Leu	Pro	
	580				585			590								
cg	cca	atc	ccc	aaa	gta	cca	gta	tct	gcc	cca	agt	tcc	agt	gat	ccc	1824
Arg	Pro	Ile	Pro	Lys	Val	Pro	Val	Ser	Ala	Pro	Ser	Ser	Ser	Asp	Pro	
	595				600				605							
tgg	aca	gga	aga	gaa	tta	acc	aac	cg	cac	tca	ctt	cca	ttt	tca	ttg	1872
Trp	Thr	Gly	Arg	Glu	Leu	Thr	Asn	Arg	His	Ser	Leu	Pro	Phe	Ser	Leu	
	610			615			620									
ccc	tca	caa	atg	gag	ccc	aga	cca	gat	gt	cct	agg	ctc	gga	agc	acg	1920
Pro	Ser	Gln	Met	Glu	Pro	Arg	Pro	Asp	Val	Pro	Arg	Leu	Gly	Ser	Thr	

625	630	635	640													
ttc	agt	ctg	gat	acc	tcc	atg	agt	atg	aat	agc	agc	cca	tta	gta	ggt	1968
Phe	Ser	Leu	Asp	Thr	Ser	Met	Ser	Met	Asn	Ser	Ser	Pro	Leu	Val	Gly	
				645				650					655			
cca	gag	tgt	gac	cac	ccc	aaa	atc	aaa	cct	tcc	tca	tct	gcc	aat	gcc	2016
Pro	Glu	Cys	Asp	His	Pro	Lys	Ile	Lys	Pro	Ser	Ser	Ser	Ala	Asn	Ala	
					660			665					670			
att	tat	tct	ctg	gct	gcc	aga	cct	cct	gtg	cca	aaa	ctg	cca	cct	2064	
Ile	Tyr	Ser	Leu	Ala	Ala	Arg	Pro	Leu	Pro	Val	Pro	Lys	Leu	Pro	Pro	
					675			680				685				
ggg	gag	caa	tgt	gag	ggt	gaa	gag	gac	aca	gag	tac	atg	act	ccc	tct	2112
Gly	Glu	Gln	Cys	Glu	Gly	Glu	Glu	Asp	Thr	Glu	Tyr	Met	Thr	Pro	Ser	
					690			695				700				
tcc	agg	cct	cta	cg	cc	tt	gat	aca	tcc	cag	agt	tca	cga	gca	tgt	2160
Ser	Arg	Pro	Leu	Arg	Pro	Leu	Asp	Thr	Ser	Gln	Ser	Ser	Arg	Ala	Cys	
					705			710			715		720			
gat	tgc	gac	cag	cag	att	gat	agc	tgt	acg	ttt	gaa	gca	atg	tat	aat	2208
Asp	Cys	Asp	Gln	Gln	Ile	Asp	Ser	Cys	Thr	Phe	Glu	Ala	Met	Tyr	Asn	
					725			730			735					
att	cag	tcc	cag	g	cc	tct	atc	acc	gag	agc	agc	acc	ttt	ggt	gaa	2256
Ile	Gln	Ser	Gln	Ala	Pro	Ser	Ile	Thr	Glu	Ser	Ser	Thr	Phe	Gly	Glu	
					740			745			750					
ggg	aat	ttt	gcc	gca	gcc	cat	gcc	aac	act	ggt	ccc	gag	gag	tca	gaa	2304
Gly	Asn	Leu	Ala	Ala	Ala	His	Ala	Asn	Thr	Gly	Pro	Glu	Glu	Ser	Glu	
					755			760			765					
aat	gag	gat	gat	ggg	tat	gat	gtc	cca	aag	cca	cct	gtg	ccg	gcc	gtg	2352
Asn	Glu	Asp	Asp	Gly	Tyr	Asp	Val	Pro	Lys	Pro	Pro	Val	Pro	Ala	Val	
					770			775			780					
ctg	gcc	cgc	cga	act	ctc	tca	gat	atc	tct	aat	gcc	agc	tcc	tcc	ttt	2400
Leu	Ala	Arg	Arg	Thr	Leu	Ser	Asp	Ile	Ser	Asn	Ala	Ser	Ser	Ser	Phe	
					785			790			795		800			
ggc	tgg	ttt	tct	ctg	gat	ggt	gat	cct	aca	aca	aat	gtc	act	gaa	ggt	2448
Gly	Trp	Leu	Ser	Leu	Asp	Gly	Asp	Pro	Thr	Thr	Asn	Val	Thr	Glu	Gly	
					805			810			815					
tcc	caa	gtt	ccc	gag	agg	cct	cca	aaa	cca	ttc	ccg	cg	aga	atc	aac	2496
Ser	Gln	Val	Pro	Glu	Arg	Pro	Pro	Lys	Pro	Phe	Pro	Arg	Arg	Ile	Asn	
					820			825			830					
tct	gaa	cg	aaa	g	ct	gg	ag	tgt	cag	caa	ggt	agt	ggt	cct	gcc	2544
Ser	Glu	Arg	Lys	Ala	Gly	Ser	Cys	Gln	Gln	Gly	Ser	Gly	Pro	Ala	Ala	
					835			840			845					
tct	gct	gcc	acc	gcc	tca	cct	cag	ctc	tcc	agt	gag	atc	gag	aac	ctc	2592
Ser	Ala	Ala	Thr	Ala	Ser	Pro	Gln	Leu	Ser	Ser	Glu	Ile	Glu	Asn	Leu	
					850			855			860					

atg agt cag ggg tac tcc tac cag gac atc cag aaa gct ttg gtc att 2640  
Met Ser Gln Gly Tyr Ser Tyr Gln Asp Ile Gln Lys Ala Leu Val Ile  
865 870 875 880

gcc cag aac aac atc gag atg gcc aaa aac atc ctc cgg gaa ttt gtt 2688  
Ala Gln Asn Asn Ile Glu Met Ala Lys Asn Ile Leu Arg Glu Phe Val  
885 890 895

tcc att tct tct cct gcc cat gta gct acc tag 2721  
Ser Ile Ser Ser Pro Ala His Val Ala Thr  
900 905

<210> 256

<211> 906

<212> PRT

<213> Artificial

<220>

<223> Synthetic Construct

<400> 256

Met Ala Gly Asn Val Lys Lys Ser Ser Gly Ala Gly Gly Gly Thr Gly  
1 5 10 15

Ser Gly Gly Ser Gly Ser Gly Leu Ile Gly Leu Met Lys Asp Ala  
20 25 30

Phe Gln Pro His His His His His His Leu Ser Pro His Pro Pro  
35 40 45

Gly Thr Val Asp Lys Lys Met Val Glu Lys Cys Trp Lys Leu Met Asp  
50 55 60

Lys Val Val Arg Leu Cys Gln Asn Pro Lys Leu Ala Leu Lys Asn Ser  
65 70 75 80

Pro Pro Tyr Ile Leu Asp Leu Leu Pro Asp Thr Tyr Gln His Leu Arg  
85 90 95

Thr Ile Leu Ser Arg Tyr Glu Gly Lys Met Glu Thr Leu Gly Glu Asn  
100 105 110

Glu Tyr Phe Arg Val Phe Met Glu Asn Leu Met Lys Lys Thr Lys Gln  
115 120 125

Thr Ile Ser Leu Phe Lys Glu Gly Lys Glu Arg Met Tyr Glu Glu Asn

130

135

140

Ser Gln Pro Arg Arg Asn Leu Thr Lys Leu Ser Leu Ile Phe Ser His  
145 150 155 160

Met Leu Ala Glu Leu Lys Gly Ile Phe Pro Ser Gly Leu Phe Gln Gly  
165 170 175

Asp Thr Phe Arg Ile Thr Lys Ala Asp Ala Ala Glu Phe Trp Arg Lys  
180 185 190

Ala Phe Gly Glu Lys Thr Ile Val Pro Trp Lys Ser Phe Arg Gln Ala  
195 200 205

Leu His Glu Val His Pro Ile Ser Ser Gly Leu Glu Ala Met Ala Leu  
210 215 220

Lys Ser Thr Ile Asp Leu Thr Cys Asn Asp Tyr Ile Ser Val Phe Glu  
225 230 235 240

Phe Asp Ile Phe Thr Arg Leu Phe Gln Pro Trp Ser Ser Leu Leu Arg  
245 250 255

Asn Trp Asn Ser Leu Ala Val Thr His Pro Gly Tyr Met Ala Phe Leu  
260 265 270

Thr Tyr Asp Glu Val Lys Ala Arg Leu Gln Lys Phe Ile His Lys Pro  
275 280 285

Gly Ser Tyr Ile Phe Arg Leu Ser Cys Thr Arg Leu Gly Gln Trp Ala  
290 295 300

Ile Gly Tyr Val Thr Ala Asp Gly Asn Ile Leu Gln Thr Ile Pro His  
305 310 315 320

Asn Lys Pro Leu Phe Gln Ala Leu Ile Asp Gly Phe Arg Glu Gly Phe  
325 330 335

Tyr Leu Phe Pro Asp Gly Arg Asn Gln Asn Pro Asp Leu Thr Gly Leu  
340 345 350

Cys Glu Pro Thr Pro Gln Asp His Ile Lys Val Thr Gln Glu Gln Tyr  
355 360 365

Glu Leu Tyr Cys Glu Met Gly Ser Thr Phe Gln Leu Cys Lys Ile Cys  
370 375 380

Ala Glu Asn Asp Lys Asp Val Lys Ile Glu Pro Cys Gly His Leu Met  
385 390 395 400

Cys Thr Ser Cys Leu Thr Ser Trp Gln Glu Ser Glu Gly Gln Gly Cys  
405 410 415

Pro Phe Cys Arg Cys Glu Ile Lys Gly Thr Glu Pro Ile Val Val Asp  
420 425 430

Pro Phe Asp Pro Arg Gly Ser Gly Ser Leu Leu Arg Gln Gly Ala Glu  
435 440 445

Gly Ala Pro Ser Pro Asn Tyr Asp Asp Asp Asp Glu Arg Ala Asp  
450 455 460

Asp Thr Leu Phe Met Met Lys Glu Leu Ala Gly Ala Lys Val Glu Arg  
465 470 475 480

Pro Pro Ser Pro Phe Ser Met Ala Pro Gln Ala Ser Leu Pro Pro Val  
485 490 495

Pro Pro Arg Leu Asp Leu Leu Pro Gln Arg Val Cys Val Pro Ser Ser  
500 505 510

Ala Ser Ala Leu Gly Thr Ala Ser Lys Ala Ala Ser Gly Ser Leu His  
515 520 525

Lys Asp Lys Pro Leu Pro Val Pro Pro Thr Leu Arg Asp Leu Pro Pro  
530 535 540

Pro Pro Pro Pro Asp Arg Pro Tyr Ser Val Gly Ala Glu Ser Arg Pro  
545 550 555 560

Gln Arg Arg Pro Leu Pro Cys Thr Pro Gly Asp Cys Pro Ser Arg Asp  
565 570 575

Lys Leu Pro Pro Val Pro Ser Ser Arg Leu Gly Asp Ser Trp Leu Pro  
580 585 590

Arg Pro Ile Pro Lys Val Pro Val Ser Ala Pro Ser Ser Ser Asp Pro  
595 600 605

Trp Thr Gly Arg Glu Leu Thr Asn Arg His Ser Leu Pro Phe Ser Leu  
610 615 620

Pro Ser Gln Met Glu Pro Arg Pro Asp Val Pro Arg Leu Gly Ser Thr  
625 630 635 640

Phe Ser Leu Asp Thr Ser Met Ser Met Asn Ser Ser Pro Leu Val Gly  
645 650 655

Pro Glu Cys Asp His Pro Lys Ile Lys Pro Ser Ser Ser Ala Asn Ala  
660 665 670

Ile Tyr Ser Leu Ala Ala Arg Pro Leu Pro Val Pro Lys Leu Pro Pro  
675 680 685

Gly Glu Gln Cys Glu Gly Glu Asp Thr Glu Tyr Met Thr Pro Ser  
690 695 700

Ser Arg Pro Leu Arg Pro Leu Asp Thr Ser Gln Ser Ser Arg Ala Cys  
705 710 715 720

Asp Cys Asp Gln Gln Ile Asp Ser Cys Thr Phe Glu Ala Met Tyr Asn  
725 730 735

Ile Gln Ser Gln Ala Pro Ser Ile Thr Glu Ser Ser Thr Phe Gly Glu  
740 745 750

Gly Asn Leu Ala Ala Ala His Ala Asn Thr Gly Pro Glu Glu Ser Glu  
755 760 765

Asn Glu Asp Asp Gly Tyr Asp Val Pro Lys Pro Pro Val Pro Ala Val  
770 775 780

Leu Ala Arg Arg Thr Leu Ser Asp Ile Ser Asn Ala Ser Ser Ser Phe  
785 790 795 800

Gly Trp Leu Ser Leu Asp Gly Asp Pro Thr Thr Asn Val Thr Glu Gly  
805 810 815

Ser Gln Val Pro Glu Arg Pro Pro Lys Pro Phe Pro Arg Arg Ile Asn  
820 825 830

Ser Glu Arg Lys Ala Gly Ser Cys Gln Gln Gly Ser Gly Pro Ala Ala  
835 840 845

Ser Ala Ala Thr Ala Ser Pro Gln Leu Ser Ser Glu Ile Glu Asn Leu  
850 855 860

Met Ser Gln Gly Tyr Ser Tyr Gln Asp Ile Gln Lys Ala Leu Val Ile  
865 870 875 880

Ala Gln Asn Asn Ile Glu Met Ala Lys Asn Ile Leu Arg Glu Phe Val  
885 890 895

Ser Ile Ser Ser Pro Ala His Val Ala Thr  
900 905

<210> 257

<211> 2721

<212> DNA

<213> Artificial

<220>

<223> c-Cbl Y774F

<220>

<221> CDS

<222> (1) ..(2718)

<400> 257

atg gcc ggc aac gtg aag aag agc tct ggg gcc ggg ggc ggc acg ggc 48  
Met Ala Gly Asn Val Lys Lys Ser Ser Gly Ala Gly Gly Gly Thr Gly  
1 5 10 15

tcc ggg ggc tcg ggt tcg ggt ggc ctg att ggg ctc atg aag gac gcc 96  
Ser Gly Gly Ser Gly Ser Gly Leu Ile Gly Leu Met Lys Asp Ala  
20 25 30

ttc cag ccg cac cac cac cac cac ctc agc ccc cac ccg ccg 144  
Phe Gln Pro His His His His His His His Leu Ser Pro His Pro Pro  
35 40 45

ggg acg gtg gac aag aag atg gtg gag aag tgc tgg aag ctc atg gac 192  
Gly Thr Val Asp Lys Lys Met Val Glu Lys Cys Trp Lys Leu Met Asp  
50 55 60

aag gtg gtg cgg ttg tgt cag aac cca aag ctg gcg cta aag aat agc 240  
Lys Val Val Arg Leu Cys Gln Asn Pro Lys Leu Ala Leu Lys Asn Ser  
65 70 75 80

cca cct tat atc tta gac ctg cta cca gat acc tac cag cat ctc cgt Pro Pro Tyr Ile Leu Asp Leu Leu Pro Asp Thr Tyr Gln His Leu Arg 85 90 95	288
act atc ttg tca aga tat gag ggg aag atg gag aca ctt gga gaa aat Thr Ile Leu Ser Arg Tyr Glu Gly Lys Met Glu Thr Leu Gly Glu Asn 100 105 110	336
gag tat ttt agg gtg ttt atg gag aat ttg atg aag aaa act aag caa Glu Tyr Phe Arg Val Phe Met Glu Asn Leu Met Lys Lys Thr Lys Gln 115 120 125	384
acc ata agc ctc ttc aag gag gga aaa gaa aga atg tat gag gag aat Thr Ile Ser Leu Phe Lys Glu Gly Lys Glu Arg Met Tyr Glu Glu Asn 130 135 140	432
tct cag cct agg cga aac cta acc aaa ctg tcc ctc atc ttc agc cac Ser Gln Pro Arg Arg Asn Leu Thr Lys Leu Ser Leu Ile Phe Ser His 145 150 155 160	480
atg ctg gca gaa cta aaa gga atc ttt cca agt gga ctc ttt cag gga Met Leu Ala Glu Leu Lys Gly Ile Phe Pro Ser Gly Leu Phe Gln Gly 165 170 175	528
gac aca ttt cgg att act aaa gca gat gct gcg gaa ttt tgg aga aaa Asp Thr Phe Arg Ile Thr Lys Ala Asp Ala Ala Glu Phe Trp Arg Lys 180 185 190	576
gct ttt ggg gaa aag aca ata gtc cct tgg aag agc ttt cga cag gct Ala Phe Gly Glu Lys Thr Ile Val Pro Trp Lys Ser Phe Arg Gln Ala 195 200 205	624
cta cat gaa gtg cat ccc atc agt tct ggg ctg gag gcc atg gct ctg Leu His Glu Val His Pro Ile Ser Ser Gly Leu Glu Ala Met Ala Leu 210 215 220	672
aaa tcc act att gat ctg acc tgc aat gat tat att tcg gtt ttt gaa Lys Ser Thr Ile Asp Leu Thr Cys Asn Asp Tyr Ile Ser Val Phe Glu 225 230 235 240	720
ttt gac atc ttt acc cga ctc ttt cag ccc tgg tcc tct ttg ctc agg Phe Asp Ile Phe Thr Arg Leu Phe Gln Pro Trp Ser Ser Leu Leu Arg 245 250 255	768
aat tgg aac agc ctt gct gta act cat cct ggc tac atg gct ttt ttg Asn Trp Asn Ser Leu Ala Val Thr His Pro Gly Tyr Met Ala Phe Leu 260 265 270	816
acg tat gac gaa gtg aaa gct cgg ctc cag aaa ttc att cac aaa cct Thr Tyr Asp Glu Val Lys Ala Arg Leu Gln Lys Phe Ile His Lys Pro 275 280 285	864
ggc agt tat atc ttc cgg ctg agc tgt act cgt ctg ggt cag tgg gct Gly Ser Tyr Ile Phe Arg Leu Ser Cys Thr Arg Leu Gly Gln Trp Ala 290 295 300	912

att ggg tat gtt act gct gat ggg aac att ctc cag aca atc cct cac Ile Gly Tyr Val Thr Ala Asp Gly Asn Ile Leu Gln Thr Ile Pro His 305 310 315 320	960
aat aaa cct ctc ttc caa gca ctg att gat ggc ttc agg gaa ggc ttc Asn Lys Pro Leu Phe Gln Ala Leu Ile Asp Gly Phe Arg Glu Gly Phe 325 330 335	1008
tat ttg ttt cct gat gga cga aat cag aat cct gat ctg act ggc tta Tyr Leu Phe Pro Asp Gly Arg Asn Gln Asn Pro Asp Leu Thr Gly Leu 340 345 350	1056
tgt gaa cca act ccc caa gac cat atc aaa gtg acc cag gaa caa tat Cys Glu Pro Thr Pro Gln Asp His Ile Lys Val Thr Gln Glu Gln Tyr 355 360 365	1104
gaa tta tac tgt gag atg ggc tcc aca ttc caa cta tgt aaa ata tgt Glu Leu Tyr Cys Glu Met Gly Ser Thr Phe Gln Leu Cys Lys Ile Cys 370 375 380	1152
gct gaa aat gat aag gat gta aag att gag ccc tgt gga cac ctc atg Ala Glu Asn Asp Lys Asp Val Lys Ile Glu Pro Cys Gly His Leu Met 385 390 395 400	1200
tgc aca tcc tgt ctt aca tcc tgg cag gaa tca gaa ggt cag ggc tgt Cys Thr Ser Cys Leu Thr Ser Trp Gln Glu Ser Glu Gly Gln Gly Cys 405 410 415	1248
cct ttc tgc cga tgt gaa att aaa ggt act gaa ccc atc gtg gta gat Pro Phe Cys Arg Cys Glu Ile Lys Gly Thr Glu Pro Ile Val Val Asp 420 425 430	1296
ccg ttt gat cct aga ggg agt ggc agc ctg ttg agg caa gga gca gag Pro Phe Asp Pro Arg Gly Ser Gly Ser Leu Leu Arg Gln Gly Ala Glu 435 440 445	1344
gga gct ccc tcc cca aat tat gat gat gat gat gaa cga gct gat Gly Ala Pro Ser Pro Asn Tyr Asp Asp Asp Asp Glu Arg Ala Asp 450 455 460	1392
gat act ctc ttc atg atg aag gaa ttg gct ggt gcc aag gtg gaa cgg Asp Thr Leu Phe Met Met Lys Glu Leu Ala Gly Ala Lys Val Glu Arg 465 470 475 480	1440
ccg cct tct cca ttc tcc atg gcc cca caa gct tcc ctt ccc ccg gtg Pro Pro Ser Pro Phe Ser Met Ala Pro Gln Ala Ser Leu Pro Pro Val 485 490 495	1488
cca cca cga ctt gac ctt ctg ccg cag cga gta tgt gtt ccc tca agt Pro Pro Arg Leu Asp Leu Leu Pro Gln Arg Val Cys Val Pro Ser Ser 500 505 510	1536
gct tct gct ctt gga act gct tct aag gct gct tct ggc tcc ctt cat Ala Ser Ala Leu Gly Thr Ala Ser Lys Ala Ala Ser Gly Ser Leu His 515 520 525	1584
aaa gac aaa cca ttg cca gta cct ccc aca ctt cga gat ctt cca cca	1632

Lys Asp Lys Pro Leu Pro Val Pro Pro Thr Leu Arg Asp Leu Pro Pro			
530	535	540	
cca ccg cct cca gac cg	cca tat tct gtt gga gca gaa tcc cga cct		1680
Pro Pro Pro Pro Asp Arg Pro Tyr Ser Val Gly Ala Glu Ser Arg Pro			
545	550	555	560
caa aga cgc ccc ttg cct tgt aca cca ggc gac tgt ccc tcc aga gac			1728
Gln Arg Arg Pro Leu Pro Cys Thr Pro Gly Asp Cys Pro Ser Arg Asp			
565	570	575	
aaa ctg ccc cct gtc ccc tct agc cgc ctt gga gac tca tgg ctg ccc			1776
Lys Leu Pro Pro Val Pro Ser Ser Arg Leu Gly Asp Ser Trp Leu Pro			
580	585	590	
cg	cca atc ccc aaa gta cca gta tct gcc cca agt tcc agt gat ccc		1824
Arg Pro Ile Pro Lys Val Pro Val Ser Ala Pro Ser Ser Ser Asp Pro			
595	600	605	
tgg aca gga aga gaa tta acc aac cg	gac cac tca ctt cca ttt tca ttg		1872
Trp Thr Gly Arg Glu Leu Thr Asn Arg His Ser Leu Pro Phe Ser Leu			
610	615	620	
ccc tca caa atg gag ccc aga cca gat gtg cct agg ctc gga agc acg			1920
Pro Ser Gln Met Glu Pro Arg Pro Asp Val Pro Arg Leu Gly Ser Thr			
625	630	635	640
ttc agt ctg gat acc tcc atg agt atg aat agc agc cca tta gta ggt			1968
Phe Ser Leu Asp Thr Ser Met Ser Met Asn Ser Ser Pro Leu Val Gly			
645	650	655	
cca gag tgt gac cac ccc aaa atc aaa cct tcc tca tct gcc aat gcc			2016
Pro Glu Cys Asp His Pro Lys Ile Lys Pro Ser Ser Ser Ala Asn Ala			
660	665	670	
att tat tct ctg gct gcc aga cct ctt cct gtg cca aaa ctg cca cct			2064
Ile Tyr Ser Leu Ala Ala Arg Pro Leu Pro Val Pro Lys Leu Pro Pro			
675	680	685	
ggg gag caa tgt gag ggt gaa gag gac aca gag tac atg act ccc tct			2112
Gly Glu Gln Cys Glu Gly Glu Glu Asp Thr Glu Tyr Met Thr Pro Ser			
690	695	700	
tcc agg cct cta cgg cct ttg gat aca tcc cag agt tca cga gca tgt			2160
Ser Arg Pro Leu Arg Pro Leu Asp Thr Ser Gln Ser Ser Arg Ala Cys			
705	710	715	720
gat tgc gac cag cag att gat agc tgt acg tat gaa gca atg tat aat			2208
Asp Cys Asp Gln Gln Ile Asp Ser Cys Thr Tyr Glu Ala Met Tyr Asn			
725	730	735	
att cag tcc cag gcg cca tct atc acc gag agc agc acc ttt ggt gaa			2256
Ile Gln Ser Gln Ala Pro Ser Ile Thr Glu Ser Ser Thr Phe Gly Glu			
740	745	750	
ggg aat ttg gcc gca gcc cat gcc aac act ggt ccc gag gag tca gaa			2304
Gly Asn Leu Ala Ala Ala His Ala Asn Thr Gly Pro Glu Glu Ser Glu			

755	760	765	
aat gag gat gat ggg ttt gat gtc cca aag cca cct gtg ccg gcc gtg Asn Glu Asp Asp Gly Phe Asp Val Pro Lys Pro Pro Val Pro Ala Val 770 775 780			2352
ctg gcc cgc cga act ctc tca gat atc tct aat gcc agc tcc tcc ttt Leu Ala Arg Arg Thr Leu Ser Asp Ile Ser Asn Ala Ser Ser Ser Phe 785 790 795 800			2400
ggc tgg ttg tct ctg gat ggt gat cct aca aca aat gtc act gaa ggt Gly Trp Leu Ser Leu Asp Gly Asp Pro Thr Thr Asn Val Thr Glu Gly 805 810 815			2448
tcc caa gtt ccc gag agg cct cca aaa cca ttc ccg ccg aga atc aac Ser Gln Val Pro Glu Arg Pro Pro Lys Pro Phe Pro Arg Arg Ile Asn 820 825 830			2496
tct gaa cgg aaa gct ggc agc tgt cag caa ggt agt ggt cct gcc gcc Ser Glu Arg Lys Ala Gly Ser Cys Gln Gln Gly Ser Gly Pro Ala Ala 835 840 845			2544
tct gct gcc acc gcc tca cct cag ctc tcc agt gag atc gag aac ctc Ser Ala Ala Thr Ala Ser Pro Gln Leu Ser Ser Glu Ile Glu Asn Leu 850 855 860			2592
atg agt cag ggg tac tcc tac cag gac atc cag aaa gct ttg gtc att Met Ser Gln Gly Tyr Ser Tyr Gln Asp Ile Gln Lys Ala Leu Val Ile 865 870 875 880			2640
gcc cag aac aac atc gag atg gcc aaa aac atc ctc ccg gaa ttt gtt Ala Gln Asn Asn Ile Glu Met Ala Lys Asn Ile Leu Arg Glu Phe Val 885 890 895			2688
tcc att tct tct cct gcc cat gta gct acc tag Ser Ile Ser Ser Pro Ala His Val Ala Thr 900 905			2721

<210> 258  
 <211> 906  
 <212> PRT  
 <213> Artificial

<220>  
 <223> Synthetic Construct

<400> 258

Met Ala Gly Asn Val Lys Lys Ser Ser Gly Ala Gly Gly Gly Thr Gly  
1 5 10 15

Ser Gly Gly Ser Gly Ser Gly Gly Leu Ile Gly Leu Met Lys Asp Ala  
20 25 30

Phe Gln Pro His His His His His His His Leu Ser Pro His Pro Pro  
35 40 45

Gly Thr Val Asp Lys Lys Met Val Glu Lys Cys Trp Lys Leu Met Asp  
50 55 60

Lys Val Val Arg Leu Cys Gln Asn Pro Lys Leu Ala Leu Lys Asn Ser  
65 70 75 80

Pro Pro Tyr Ile Leu Asp Leu Leu Pro Asp Thr Tyr Gln His Leu Arg  
85 90 95

Thr Ile Leu Ser Arg Tyr Glu Gly Lys Met Glu Thr Leu Gly Glu Asn  
100 105 110

Glu Tyr Phe Arg Val Phe Met Glu Asn Leu Met Lys Lys Thr Lys Gln  
115 120 125

Thr Ile Ser Leu Phe Lys Glu Gly Lys Glu Arg Met Tyr Glu Glu Asn  
130 135 140

Ser Gln Pro Arg Arg Asn Leu Thr Lys Leu Ser Leu Ile Phe Ser His  
145 150 155 160

Met Leu Ala Glu Leu Lys Gly Ile Phe Pro Ser Gly Leu Phe Gln Gly  
165 170 175

Asp Thr Phe Arg Ile Thr Lys Ala Asp Ala Ala Glu Phe Trp Arg Lys  
180 185 190

Ala Phe Gly Glu Lys Thr Ile Val Pro Trp Lys Ser Phe Arg Gln Ala  
195 200 205

Leu His Glu Val His Pro Ile Ser Ser Gly Leu Glu Ala Met Ala Leu  
210 215 220

Lys Ser Thr Ile Asp Leu Thr Cys Asn Asp Tyr Ile Ser Val Phe Glu  
225 230 235 240

Phe Asp Ile Phe Thr Arg Leu Phe Gln Pro Trp Ser Ser Leu Leu Arg  
245 250 255

Asn Trp Asn Ser Leu Ala Val Thr His Pro Gly Tyr Met Ala Phe Leu

260

265

270

Thr Tyr Asp Glu Val Lys Ala Arg Leu Gln Lys Phe Ile His Lys Pro  
275 280 285

Gly Ser Tyr Ile Phe Arg Leu Ser Cys Thr Arg Leu Gly Gln Trp Ala  
290 295 300

Ile Gly Tyr Val Thr Ala Asp Gly Asn Ile Leu Gln Thr Ile Pro His  
305 310 315 320

Asn Lys Pro Leu Phe Gln Ala Leu Ile Asp Gly Phe Arg Glu Gly Phe  
325 330 335

Tyr Leu Phe Pro Asp Gly Arg Asn Gln Asn Pro Asp Leu Thr Gly Leu  
340 345 350

Cys Glu Pro Thr Pro Gln Asp His Ile Lys Val Thr Gln Glu Gln Tyr  
355 360 365

Glu Leu Tyr Cys Glu Met Gly Ser Thr Phe Gln Leu Cys Lys Ile Cys  
370 375 380

Ala Glu Asn Asp Lys Asp Val Lys Ile Glu Pro Cys Gly His Leu Met  
385 390 395 400

Cys Thr Ser Cys Leu Thr Ser Trp Gln Glu Ser Glu Gly Gln Gly Cys  
405 410 415

Pro Phe Cys Arg Cys Glu Ile Lys Gly Thr Glu Pro Ile Val Val Asp  
420 425 430

Pro Phe Asp Pro Arg Gly Ser Gly Ser Leu Leu Arg Gln Gly Ala Glu  
435 440 445

Gly Ala Pro Ser Pro Asn Tyr Asp Asp Asp Asp Glu Arg Ala Asp  
450 455 460

Asp Thr Leu Phe Met Met Lys Glu Leu Ala Gly Ala Lys Val Glu Arg  
465 470 475 480

Pro Pro Ser Pro Phe Ser Met Ala Pro Gln Ala Ser Leu Pro Pro Val  
485 490 495

Pro Pro Arg Leu Asp Leu Leu Pro Gln Arg Val Cys Val Pro Ser Ser  
500 505 510

Ala Ser Ala Leu Gly Thr Ala Ser Lys Ala Ala Ser Gly Ser Leu His  
515 520 525

Lys Asp Lys Pro Leu Pro Val Pro Pro Thr Leu Arg Asp Leu Pro Pro  
530 535 540

Pro Pro Pro Pro Asp Arg Pro Tyr Ser Val Gly Ala Glu Ser Arg Pro  
545 550 555 560

Gln Arg Arg Pro Leu Pro Cys Thr Pro Gly Asp Cys Pro Ser Arg Asp  
565 570 575

Lys Leu Pro Pro Val Pro Ser Ser Arg Leu Gly Asp Ser Trp Leu Pro  
580 585 590

Arg Pro Ile Pro Lys Val Pro Val Ser Ala Pro Ser Ser Ser Asp Pro  
595 600 605

Trp Thr Gly Arg Glu Leu Thr Asn Arg His Ser Leu Pro Phe Ser Leu  
610 615 620

Pro Ser Gln Met Glu Pro Arg Pro Asp Val Pro Arg Leu Gly Ser Thr  
625 630 635 640

Phe Ser Leu Asp Thr Ser Met Ser Met Asn Ser Ser Pro Leu Val Gly  
645 650 655

Pro Glu Cys Asp His Pro Lys Ile Lys Pro Ser Ser Ser Ala Asn Ala  
660 665 670

Ile Tyr Ser Leu Ala Ala Arg Pro Leu Pro Val Pro Lys Leu Pro Pro  
675 680 685

Gly Glu Gln Cys Glu Gly Glu Glu Asp Thr Glu Tyr Met Thr Pro Ser  
690 695 700

Ser Arg Pro Leu Arg Pro Leu Asp Thr Ser Gln Ser Ser Arg Ala Cys  
705 710 715 720

Asp Cys Asp Gln Gln Ile Asp Ser Cys Thr Tyr Glu Ala Met Tyr Asn  
725 730 735

Ile Gln Ser Gln Ala Pro Ser Ile Thr Glu Ser Ser Thr Phe Gly Glu  
740 745 750

Gly Asn Leu Ala Ala Ala His Ala Asn Thr Gly Pro Glu Glu Ser Glu  
755 760 765

Asn Glu Asp Asp Gly Phe Asp Val Pro Lys Pro Pro Val Pro Ala Val  
770 775 780

Leu Ala Arg Arg Thr Leu Ser Asp Ile Ser Asn Ala Ser Ser Ser Phe  
785 790 795 800

Gly Trp Leu Ser Leu Asp Gly Asp Pro Thr Thr Asn Val Thr Glu Gly  
805 810 815

Ser Gln Val Pro Glu Arg Pro Pro Lys Pro Phe Pro Arg Arg Ile Asn  
820 825 830

Ser Glu Arg Lys Ala Gly Ser Cys Gln Gln Gly Ser Gly Pro Ala Ala  
835 840 845

Ser Ala Ala Thr Ala Ser Pro Gln Leu Ser Ser Glu Ile Glu Asn Leu  
850 855 860

Met Ser Gln Gly Tyr Ser Tyr Gln Asp Ile Gln Lys Ala Leu Val Ile  
865 870 875 880

Ala Gln Asn Asn Ile Glu Met Ala Lys Asn Ile Leu Arg Glu Phe Val  
885 890 895

Ser Ile Ser Ser Pro Ala His Val Ala Thr  
900 905

<210> 259  
<211> 2721  
<212> DNA  
<213> Artificial

<220>  
<223> c-Cbl, Y700F/Y731F/Y774F

<220>  
<221> CDS  
<222> (1) . . (2718)

<400> 259  
 atg gcc ggc aac gtg aag aag agc tct ggg gcc ggg ggc ggc acg ggc 48  
 Met Ala Gly Asn Val Lys Lys Ser Ser Gly Ala Gly Gly Gly Thr Gly  
 1 5 10 15  
  
 tcc ggg ggc tcg ggt tcg ggt ggc ctg att ggg ctc atg aag gac gcc 96  
 Ser Gly Gly Ser Gly Ser Gly Leu Ile Gly Leu Met Lys Asp Ala  
 20 25 30  
  
 ttc cag ccg cac cac cac cac cac ctc agc ccc cac ccg ccg 144  
 Phe Gln Pro His His His His His His Leu Ser Pro His Pro Pro  
 35 40 45  
  
 ggg acg gtg gac aag aag atg gtg gag aag tgc tgg aag ctc atg gac 192  
 Gly Thr Val Asp Lys Lys Met Val Glu Lys Cys Trp Lys Leu Met Asp  
 50 55 60  
  
 aag gtg gtg cgg ttg tgt cag aac cca aag ctg gcg cta aag aat agc 240  
 Lys Val Val Arg Leu Cys Gln Asn Pro Lys Leu Ala Leu Lys Asn Ser  
 65 70 75 80  
  
 cca cct tat atc tta gac ctg cta cca gat acc tac cag cat ctc cgt 288  
 Pro Pro Tyr Ile Leu Asp Leu Leu Pro Asp Thr Tyr Gln His Leu Arg  
 85 90 95  
  
 act atc ttg tca aga tat gag ggg aag atg gag aca ctt gga gaa aat 336  
 Thr Ile Leu Ser Arg Tyr Glu Gly Lys Met Glu Thr Leu Gly Glu Asn  
 100 105 110  
  
 gag tat ttt agg gtg ttt atg gag aat ttg atg aag aaa act aag caa 384  
 Glu Tyr Phe Arg Val Phe Met Glu Asn Leu Met Lys Lys Thr Lys Gln  
 115 120 125  
  
 acc ata agc ctc ttc aag gag gga aaa gaa aga atg tat gag gag aat 432  
 Thr Ile Ser Leu Phe Lys Glu Gly Lys Glu Arg Met Tyr Glu Glu Asn  
 130 135 140  
  
 tct cag cct agg cga aac cta acc aaa ctg tcc ctc atc ttc agc cac 480  
 Ser Gln Pro Arg Arg Asn Leu Thr Lys Leu Ser Leu Ile Phe Ser His  
 145 150 155 160  
  
 atg ctg gca gaa cta aaa gga atc ttt cca agt gga ctc ttt cag gga 528  
 Met Leu Ala Glu Leu Lys Gly Ile Phe Pro Ser Gly Leu Phe Gln Gly  
 165 170 175  
  
 gac aca ttt cgg att act aaa gca gat gct gcg gaa ttt tgg aga aaa 576  
 Asp Thr Phe Arg Ile Thr Lys Ala Asp Ala Ala Glu Phe Trp Arg Lys  
 180 185 190  
  
 gct ttt ggg gaa aag aca ata gtc cct tgg aag agc ttt cga cag gct 624  
 Ala Phe Gly Glu Lys Thr Ile Val Pro Trp Lys Ser Phe Arg Gln Ala  
 195 200 205

cta cat gaa gtg cat ccc atc agt tct ggg ctg gag gcc atg gct ctg	672
Leu His Glu Val His Pro Ile Ser Ser Gly Leu Glu Ala Met Ala Leu	
210 215 220	
aaa tcc act att gat ctg acc tgc aat gat tat att tcg gtt ttt gaa	720
Lys Ser Thr Ile Asp Leu Thr Cys Asn Asp Tyr Ile Ser Val Phe Glu	
225 230 235 240	
ttt gac atc ttt acc cga ctc ttt cag ccc tgg tcc tct ttg ctc agg	768
Phe Asp Ile Phe Thr Arg Leu Phe Gln Pro Trp Ser Ser Leu Leu Arg	
245 250 255	
aat tgg aac agc ctt gct gta act cat cct ggc tac atg gct ttt ttg	816
Asn Trp Asn Ser Leu Ala Val Thr His Pro Gly Tyr Met Ala Phe Leu	
260 265 270	
acg tat gac gaa gtg aaa gct cgg ctc cag aaa ttc att cac aaa cct	864
Thr Tyr Asp Glu Val Lys Ala Arg Leu Gln Lys Phe Ile His Lys Pro	
275 280 285	
ggc agt tat atc ttc cgg ctg agc tgt act cgt ctg ggt cag tgg gct	912
Gly Ser Tyr Ile Phe Arg Leu Ser Cys Thr Arg Leu Gly Gln Trp Ala	
290 295 300	
att ggg tat gtt act gct gat ggg aac att ctc cag aca atc cct cac	960
Ile Gly Tyr Val Thr Ala Asp Gly Asn Ile Leu Gln Thr Ile Pro His	
305 310 315 320	
aat aaa cct ctc ttccaa gca ctg att gat ggc ttc agg gaa ggc ttc	1008
Asn Lys Pro Leu Phe Gln Ala Leu Ile Asp Gly Phe Arg Glu Gly Phe	
325 330 335	
tat ttg ttt cct gat gga cga aat cag aat cct gat ctg act ggc tta	1056
Tyr Leu Phe Pro Asp Gly Arg Asn Gln Asn Pro Asp Leu Thr Gly Leu	
340 345 350	
tgt gaa cca act ccc caa gac cat atc aaa gtg acc cag gaa caa tat	1104
Cys Glu Pro Thr Pro Gln Asp His Ile Lys Val Thr Gln Glu Gln Tyr	
355 360 365	
gaa tta tac tgt gag atg ggc tcc aca ttc caa cta tgt aaa ata tgt	1152
Glu Leu Tyr Cys Glu Met Gly Ser Thr Phe Gln Leu Cys Lys Ile Cys	
370 375 380	
gct gaa aat gat aag gat gta aag att gag ccc tgt gga cac ctc atg	1200
Ala Glu Asn Asp Lys Asp Val Lys Ile Glu Pro Cys Gly His Leu Met	
385 390 395 400	
tgc aca tcc tgt ctt aca tcc tgg cag gaa tca gaa ggt cag ggc tgt	1248
Cys Thr Ser Cys Leu Thr Ser Trp Gln Glu Ser Glu Gly Gln Gly Cys	
405 410 415	
cct ttc tgc cga tgt gaa att aaa ggt act gaa ccc atc gtg gta gat	1296
Pro Phe Cys Arg Cys Glu Ile Lys Gly Thr Glu Pro Ile Val Val Asp	
420 425 430	

ccg ttt gat cct aga ggg agt ggc agc ctg ttg agg caa gga gca gag Pro Phe Asp Pro Arg Gly Ser Gly Ser Leu Leu Arg Gln Gly Ala Glu 435 440 445	1344
gga gct ccc tcc cca aat tat gat gat gat gat gaa cga gct gat Gly Ala Pro Ser Pro Asn Tyr Asp Asp Asp Asp Glu Arg Ala Asp 450 455 460	1392
gat act ctc ttc atg atg aag gaa ttg gct ggt gcc aag gtg gaa cgg Asp Thr Leu Phe Met Met Lys Glu Leu Ala Gly Ala Lys Val Glu Arg 465 470 475 480	1440
ccg cct tct cca ttc tcc atg gcc cca caa gct tcc ctt ccc ccc gtg Pro Pro Ser Pro Phe Ser Met Ala Pro Gln Ala Ser Leu Pro Pro Val 485 490 495	1488
cca cca cga ctt gac ctt ctg ccg cag cga gta tgt gtt ccc tca agt Pro Pro Arg Leu Asp Leu Leu Pro Gln Arg Val Cys Val Pro Ser Ser 500 505 510	1536
gct tct gct ctt gga act gct tct aag gct gct tct ggc tcc ctt cat Ala Ser Ala Leu Gly Thr Ala Ser Lys Ala Ala Ser Gly Ser Leu His 515 520 525	1584
aaa gac aaa cca ttg cca gta cct ccc aca ctt cga gat ctt cca cca Lys Asp Lys Pro Leu Pro Val Pro Pro Thr Leu Arg Asp Leu Pro Pro 530 535 540	1632
cca ccg cct cca gac ccg cca tat tct gtt gga gca gaa tcc cga cct Pro Pro Pro Pro Asp Arg Pro Tyr Ser Val Gly Ala Glu Ser Arg Pro 545 550 555 560	1680
caa aga cgc ccc ttg cct tgt aca cca ggc gac tgt ccc tcc aga gac Gln Arg Arg Pro Leu Pro Cys Thr Pro Gly Asp Cys Pro Ser Arg Asp 565 570 575	1728
aaa ctg ccc cct gtc ccc tct agc cgc ctt gga gac tca tgg ctg ccc Lys Leu Pro Pro Val Pro Ser Ser Arg Leu Gly Asp Ser Trp Leu Pro 580 585 590	1776
cg <sup>g</sup> cca atc ccc aaa gta cca gta tct gcc cca agt tcc agt gat ccc Arg Pro Ile Pro Lys Val Pro Val Ser Ala Pro Ser Ser Asp Pro 595 600 605	1824
tgg aca gga aga gaa tta acc aac ccg cac tca ctt cca ttt tca ttg Trp Thr Gly Arg Glu Leu Thr Asn Arg His Ser Leu Pro Phe Ser Leu 610 615 620	1872
ccc tca caa atg gag ccc aga cca gat gtg cct agg ctc gga agc acg Pro Ser Gln Met Glu Pro Arg Pro Asp Val Pro Arg Leu Gly Ser Thr 625 630 635 640	1920
ttc agt ctg gat acc tcc atg agt aat agc agc cca tta gta ggt Phe Ser Leu Asp Thr Ser Met Ser Met Asn Ser Ser Pro Leu Val Gly 645 650 655	1968
cca gag tgt gac cac ccc aaa atc aaa cct tcc tca tct gcc aat gcc	2016

Pro	Glu	Cys	Asp	His	Pro	Lys	Ile	Lys	Pro	Ser	Ser	Ser	Ala	Asn	Ala	
660					665				670							
att tat tct ctg gct gcc aga cct ctt cct gtg cca aaa ctg cca cct															2064	
Ile	Tyr	Ser	Leu	Ala	Ala	Arg	Pro	Leu	Pro	Val	Pro	Lys	Leu	Pro	Pro	
675				680				685								
ggg gag caa tgt gag ggt gaa gag gac aca gag ttc atg act ccc tct															2112	
Gly	Glu	Gln	Cys	Glu	Gly	Glu	Asp	Thr	Glu	Phe	Met	Thr	Pro	Ser		
690				695				700								
tcc agg cct cta cgg cct ttg gat aca tcc cag agt tca cga gca tgt															2160	
Ser	Arg	Pro	Leu	Arg	Pro	Leu	Asp	Thr	Ser	Gln	Ser	Ser	Arg	Ala	Cys	
705				710				715		720						
gat tgc gac cag cag att gat agc tgt acg ttt gaa gca atg tat aat															2208	
Asp	Cys	Asp	Gln	Gln	Ile	Asp	Ser	Cys	Thr	Phe	Glu	Ala	Met	Tyr	Asn	
725					730				735							
att cag tcc cag gcg cca tct atc acc gag agc agc acc ttt ggt gaa															2256	
Ile	Gln	Ser	Gln	Ala	Pro	Ser	Ile	Thr	Glu	Ser	Ser	Thr	Phe	Gly	Glu	
740					745				750							
ggg aat ttg gcc gca gcc cat gcc aac act ggt ccc gag gag tca gaa															2304	
Gly	Asn	Leu	Ala	Ala	Ala	His	Ala	Asn	Thr	Gly	Pro	Glu	Ser	Glu		
755					760				765							
aat gag gat gat ggg ttt gat gtc cca aag cca cct gtg ccg gcc gtg															2352	
Asn	Glu	Asp	Asp	Gly	Phe	Asp	Val	Pro	Lys	Pro	Pro	Val	Pro	Ala	Val	
770				775				780								
ctg gcc cgc cga act ctc tca gat atc tct aat gcc agc tcc tcc ttt															2400	
Leu	Ala	Arg	Arg	Thr	Leu	Ser	Asp	Ile	Ser	Asn	Ala	Ser	Ser	Ser	Phe	
785					790			795		800						
ggc tgg ttg tct ctg gat ggt gat cct aca aca aat gtc act gaa ggt															2448	
Gly	Trp	Leu	Ser	Leu	Asp	Gly	Asp	Pro	Thr	Thr	Asn	Val	Thr	Glu	Gly	
					805			810		815						
tcc caa gtt ccc gag agg cct cca aaa cca ttc ccg cggt aga atc aac															2496	
Ser	Gln	Val	Pro	Glu	Arg	Pro	Pro	Lys	Pro	Phe	Pro	Arg	Arg	Ile	Asn	
820				825				830								
tct gaa cgg aaa gct ggc agc tgt cag caa ggt agt ggt cct gcc gcc															2544	
Ser	Glu	Arg	Lys	Ala	Gly	Ser	Cys	Gln	Gln	Gly	Ser	Gly	Pro	Ala	Ala	
835				840				845								
tct gct gcc acc gcc tca cct cag ctc tcc agt gag atc gag aac ctc															2592	
Ser	Ala	Ala	Thr	Ala	Ser	Pro	Gln	Leu	Ser	Ser	Glu	Ile	Glu	Asn	Leu	
850				855				860								
atg agt cag ggg tac tcc tac cag gac atc cag aaa gct ttg gtc att															2640	
Met	Ser	Gln	Gly	Tyr	Ser	Tyr	Gln	Asp	Ile	Gln	Lys	Ala	Leu	Val	Ile	
865					870			875		880						
gcc cag aac aac atc gag atg gcc aaa aac atc ctc ccg gaa ttt gtt															2688	
Ala	Gln	Asn	Asn	Ile	Glu	Met	Ala	Lys	Asn	Ile	Leu	Arg	Glu	Phe	Val	

885

890

895

tcc att tct tct cct gcc cat gta gct acc tag  
Ser Ile Ser Ser Pro Ala His Val Ala Thr  
900 905

2721

<210> 260  
<211> 906  
<212> PRT  
<213> Artificial

<220>  
<223> Synthetic Construct

<400> 260

Met Ala Gly Asn Val Lys Lys Ser Ser Gly Ala Gly Gly Gly Thr Gly  
1 5 10 15

Ser Gly Gly Ser Gly Ser Gly Gly Leu Ile Gly Leu Met Lys Asp Ala  
20 25 30

Phe Gln Pro His His His His His His Leu Ser Pro His Pro Pro  
35 40 45

Gly Thr Val Asp Lys Lys Met Val Glu Lys Cys Trp Lys Leu Met Asp  
50 55 60

Lys Val Val Arg Leu Cys Gln Asn Pro Lys Leu Ala Leu Lys Asn Ser  
65 70 75 80

Pro Pro Tyr Ile Leu Asp Leu Leu Pro Asp Thr Tyr Gln His Leu Arg  
85 90 95

Thr Ile Leu Ser Arg Tyr Glu Gly Lys Met Glu Thr Leu Gly Glu Asn  
100 105 110

Glu Tyr Phe Arg Val Phe Met Glu Asn Leu Met Lys Lys Thr Lys Gln  
115 120 125

Thr Ile Ser Leu Phe Lys Glu Gly Lys Glu Arg Met Tyr Glu Glu Asn  
130 135 140

Ser Gln Pro Arg Arg Asn Leu Thr Lys Leu Ser Leu Ile Phe Ser His  
145 150 155 160

Met Leu Ala Glu Leu Lys Gly Ile Phe Pro Ser Gly Leu Phe Gln Gly  
165 170 175

Asp Thr Phe Arg Ile Thr Lys Ala Asp Ala Ala Glu Phe Trp Arg Lys  
180 185 190

Ala Phe Gly Glu Lys Thr Ile Val Pro Trp Lys Ser Phe Arg Gln Ala  
195 200 205

Leu His Glu Val His Pro Ile Ser Ser Gly Leu Glu Ala Met Ala Leu  
210 215 220

Lys Ser Thr Ile Asp Leu Thr Cys Asn Asp Tyr Ile Ser Val Phe Glu  
225 230 235 240

Phe Asp Ile Phe Thr Arg Leu Phe Gln Pro Trp Ser Ser Leu Leu Arg  
245 250 255

Asn Trp Asn Ser Leu Ala Val Thr His Pro Gly Tyr Met Ala Phe Leu  
260 265 270

Thr Tyr Asp Glu Val Lys Ala Arg Leu Gln Lys Phe Ile His Lys Pro  
275 280 285

Gly Ser Tyr Ile Phe Arg Leu Ser Cys Thr Arg Leu Gly Gln Trp Ala  
290 295 300

Ile Gly Tyr Val Thr Ala Asp Gly Asn Ile Leu Gln Thr Ile Pro His  
305 310 315 320

Asn Lys Pro Leu Phe Gln Ala Leu Ile Asp Gly Phe Arg Glu Gly Phe  
325 330 335

Tyr Leu Phe Pro Asp Gly Arg Asn Gln Asn Pro Asp Leu Thr Gly Leu  
340 345 350

Cys Glu Pro Thr Pro Gln Asp His Ile Lys Val Thr Gln Glu Gln Tyr  
355 360 365

Glu Leu Tyr Cys Glu Met Gly Ser Thr Phe Gln Leu Cys Lys Ile Cys  
370 375 380

Ala Glu Asn Asp Lys Asp Val Lys Ile Glu Pro Cys Gly His Leu Met

385

390

395

400

Cys Thr Ser Cys Leu Thr Ser Trp Gln Glu Ser Glu Gly Gln Gly Cys  
405 410 415

Pro Phe Cys Arg Cys Glu Ile Lys Gly Thr Glu Pro Ile Val Val Asp  
420 425 430

Pro Phe Asp Pro Arg Gly Ser Gly Ser Leu Leu Arg Gln Gly Ala Glu  
435 440 445

Gly Ala Pro Ser Pro Asn Tyr Asp Asp Asp Asp Glu Arg Ala Asp  
450 455 460

Asp Thr Leu Phe Met Met Lys Glu Leu Ala Gly Ala Lys Val Glu Arg  
465 470 475 480

Pro Pro Ser Pro Phe Ser Met Ala Pro Gln Ala Ser Leu Pro Pro Val  
485 490 495

Pro Pro Arg Leu Asp Leu Leu Pro Gln Arg Val Cys Val Pro Ser Ser  
500 505 510

Ala Ser Ala Leu Gly Thr Ala Ser Lys Ala Ala Ser Gly Ser Leu His  
515 520 525

Lys Asp Lys Pro Leu Pro Val Pro Pro Thr Leu Arg Asp Leu Pro Pro  
530 535 540

Pro Pro Pro Pro Asp Arg Pro Tyr Ser Val Gly Ala Glu Ser Arg Pro  
545 550 555 560

Gln Arg Arg Pro Leu Pro Cys Thr Pro Gly Asp Cys Pro Ser Arg Asp  
565 570 575

Lys Leu Pro Pro Val Pro Ser Ser Arg Leu Gly Asp Ser Trp Leu Pro  
580 585 590

Arg Pro Ile Pro Lys Val Pro Val Ser Ala Pro Ser Ser Ser Asp Pro  
595 600 605

Trp Thr Gly Arg Glu Leu Thr Asn Arg His Ser Leu Pro Phe Ser Leu  
610 615 620

Pro Ser Gln Met Glu Pro Arg Pro Asp Val Pro Arg Leu Gly Ser Thr  
625 630 635 640

Phe Ser Leu Asp Thr Ser Met Ser Met Asn Ser Ser Pro Leu Val Gly  
645 650 655

Pro Glu Cys Asp His Pro Lys Ile Lys Pro Ser Ser Ala Asn Ala  
660 665 670

Ile Tyr Ser Leu Ala Ala Arg Pro Leu Pro Val Pro Lys Leu Pro Pro  
675 680 685

Gly Glu Gln Cys Glu Gly Glu Glu Asp Thr Glu Phe Met Thr Pro Ser  
690 695 700

Ser Arg Pro Leu Arg Pro Leu Asp Thr Ser Gln Ser Ser Arg Ala Cys  
705 710 715 720

Asp Cys Asp Gln Gln Ile Asp Ser Cys Thr Phe Glu Ala Met Tyr Asn  
725 730 735

Ile Gln Ser Gln Ala Pro Ser Ile Thr Glu Ser Ser Thr Phe Gly Glu  
740 745 750

Gly Asn Leu Ala Ala Ala His Ala Asn Thr Gly Pro Glu Glu Ser Glu  
755 760 765

Asn Glu Asp Asp Gly Phe Asp Val Pro Lys Pro Pro Val Pro Ala Val  
770 775 780

Leu Ala Arg Arg Thr Leu Ser Asp Ile Ser Asn Ala Ser Ser Ser Phe  
785 790 795 800

Gly Trp Leu Ser Leu Asp Gly Asp Pro Thr Thr Asn Val Thr Glu Gly  
805 810 815

Ser Gln Val Pro Glu Arg Pro Pro Lys Pro Phe Pro Arg Arg Ile Asn  
820 825 830

Ser Glu Arg Lys Ala Gly Ser Cys Gln Gln Gly Ser Gly Pro Ala Ala  
835 840 845

Ser Ala Ala Thr Ala Ser Pro Gln Leu Ser Ser Glu Ile Glu Asn Leu  
850 855 860

Met Ser Gln Gly Tyr Ser Tyr Gln Asp Ile Gln Lys Ala Leu Val Ile  
865 870 875 880

Ala Gln Asn Asn Ile Glu Met Ala Lys Asn Ile Leu Arg Glu Phe Val  
885 890 895

Ser Ile Ser Ser Pro Ala His Val Ala Thr  
900 905

<210> 261

<211> 1443

<212> DNA

<213> Artificial

<220>

<223> c-Cbl 480

<220>

<221> CDS

<222> (1)...(1440)

<400> 261

atg gcc ggc aac gtg aag aag agc tct ggg gcc ggg ggc ggc acg ggc 48  
Met Ala Gly Asn Val Lys Lys Ser Ser Gly Ala Gly Gly Gly Thr Gly  
1 5 10 15

tcc ggg ggc tcg ggt tcg ggt ggc ctg att ggg ctc atg aag gac gcc 96  
Ser Gly Gly Ser Gly Gly Leu Ile Gly Leu Met Lys Asp Ala  
20 25 30

ttc cag ccg cac cac cac cac cac ctc agc ccc cac ccg ccg 144  
Phe Gln Pro His His His His His His Leu Ser Pro His Pro Pro  
35 40 45

ggg acg gtg gac aag aag atg gtg gag aag tgc tgg aag ctc atg gac 192  
Gly Thr Val Asp Lys Lys Met Val Glu Lys Cys Trp Lys Leu Met Asp  
50 55 60

aag gtg gtg cgg ttg tgt cag aac cca aag ctg gcg cta aag aat agc 240  
Lys Val Val Arg Leu Cys Gln Asn Pro Lys Leu Ala Leu Lys Asn Ser  
65 70 75 80

cca cct tat atc tta gac ctg cta cca gat acc tac cag cat ctc cgt 288  
Pro Pro Tyr Ile Leu Asp Leu Leu Pro Asp Thr Tyr Gln His Leu Arg  
85 90 95

act atc ttg tca aga tat gag ggg aag atg gag aca ctt gga gaa aat 336  
Thr Ile Leu Ser Arg Tyr Glu Gly Lys Met Glu Thr Leu Gly Glu Asn

100	105	110	
gag tat ttt agg gtg ttt atg gag aat ttg atg aag aaa act aag caa, Glu Tyr Phe Arg Val Phe Met Glu Asn Leu Met Lys Lys Thr Lys Gln			384
115	120	125	
acc ata agc ctc ttc aag gag gga aaa gaa aga atg tat gag gag aat Thr Ile Ser Leu Phe Lys Glu Gly Lys Glu Arg Met Tyr Glu Glu Asn			432
130	135	140	
tct cag cct agg cga aac cta acc aaa ctg tcc ctc atc ttc agc cac Ser Gln Pro Arg Arg Asn Leu Thr Lys Leu Ser Leu Ile Phe Ser His			480
145	150	155	160
atg ctg gca gaa cta aaa gga atc ttt cca agt gga ctc ttt cag gga Met Leu Ala Glu Leu Lys Gly Ile Phe Pro Ser Gly Leu Phe Gln Gly			528
165	170	175	
gac aca ttt cgg att act aaa gca gat gct gcg gaa ttt tgg aga aaa Asp Thr Phe Arg Ile Thr Lys Ala Asp Ala Ala Glu Phe Trp Arg Lys			576
180	185	190	
gct ttt ggg gaa aag aca ata gtc cct tgg aag agc ttt cga cag gct Ala Phe Gly Glu Lys Thr Ile Val Pro Trp Lys Ser Phe Arg Gln Ala			624
195	200	205	
cta cat gaa gtg cat ccc atc agt tct ggg ctg gag gcc atg gct ctg Leu His Glu Val His Pro Ile Ser Ser Gly Leu Glu Ala Met Ala Leu			672
210	215	220	
aaa tcc act att gat ctg acc tgc aat gat tat att tcg gtt ttt gaa Lys Ser Thr Ile Asp. Leu Thr Cys Asn Asp Tyr Ile Ser Val Phe Glu			720
225	230	235	240
ttt gac atc ttt acc cga ctc ttt cag ccc tgg tcc tct ttg ctc agg Phe Asp Ile Phe Thr Arg Leu Phe Gln Pro Trp Ser Ser Leu Leu Arg			768
245	250	255	
aat tgg aac agc ctt gct gta act cat cct ggc tac atg gct ttt ttg Asn Trp Asn Ser Leu Ala Val Thr His Pro Gly Tyr Met Ala Phe Leu			816
260	265	270	
acg tat gac gaa gtg aaa gct cgg ctc cag aaa ttc att cac aaa cct Thr Tyr Asp Glu Val Lys Ala Arg Leu Gln Lys Phe Ile His Lys Pro			864
275	280	285	
ggc agt tat atc ttc cgg ctg agc tgt act cgt ctg ggt, cag tgg gct Gly Ser Tyr Ile Phe Arg Leu Ser Cys Thr Arg Leu Gly Gln Trp Ala			912
290	295	300	
att ggg tat gtt act gct gat ggg aac att ctc cag aca atc cct cac Ile Gly Tyr Val Thr Ala Asp Gly Asn Ile Leu Gln Thr Ile Pro His			960
305	310	315	320
aat aaa cct ctc ttc caa gca ctg att gat ggc ttc agg gaa ggc ttc Asn Lys Pro Leu Phe Gln Ala Leu Ile Asp Gly Phe Arg Glu Gly Phe			1008
325	330	335	

tat ttg ttt cct gat gga cga aat cag aat cct gat ctg act ggc tta	1056
Tyr Leu Phe Pro Asp Gly Arg Asn Gln Asn Pro Asp Leu Thr Gly Leu	
340 345 350	
tgt gaa cca act ccc caa gac cat atc aaa gtg acc cag gaa caa tat	1104
Cys Glu Pro Thr Pro Gln Asp His Ile Lys Val Thr Gln Glu Gln Tyr	
355 360 365	
gaa tta tac tgt gag atg ggc tcc aca ttc caa cta tgt aaa ata tgt	1152
Glu Leu Tyr Cys Glu Met Gly Ser Thr Phe Gln Leu Cys Lys Ile Cys	
370 375 380	
gct gaa aat gat aag gat gta aag att gag ccc tgt gga cac ctc atg	1200
Ala Glu Asn Asp Lys Asp Val Lys Ile Glu Pro Cys Gly His Leu Met	
385 390 395 400	
tgc aca tcc tgt ctt aca tcc tgg cag gaa tca gaa ggt cag ggc tgt	1248
Cys Thr Ser Cys Leu Thr Ser Trp Gln Glu Ser Glu Gly Gln Gly Cys	
405 410 415	
cct ttc tgc cga tgt gaa att aaa ggt act gaa ccc atc gtg gta gat	1296
Pro Phe Cys Arg Cys Glu Ile Lys Gly Thr Glu Pro Ile Val Val Asp	
420 425 430	
ccg ttt gat cct aga ggg agt ggc agc ctg ttg agg caa gga gca gag	1344
Pro Phe Asp Pro Arg Gly Ser Gly Ser Leu Leu Arg Gln Gly Ala Glu	
435 440 445	
gga gct ccc tcc cca aat tat gat gat gat gat gaa cga gct gat	1392
Gly Ala Pro Ser Pro Asn Tyr Asp Asp Asp Asp Glu Arg Ala Asp	
450 455 460	
gat act ctc ttc atg atg aag gaa ttg gct ggt gcc aag gtg gaa cgg	1440
Asp Thr Leu Phe Met Met Lys Glu Leu Ala Gly Ala Lys Val Glu Arg	
465 470 475 480	
tag	1443

<210> 262  
<211> 480  
<212> PRT  
<213> Artificial

<220>  
<223> Synthetic Construct

<400> 262

Met Ala Gly Asn Val Lys Lys Ser Ser Gly Ala Gly Gly Gly Thr Gly  
1 5 10 15

Ser Gly Gly Ser Gly Ser Gly Leu Ile Gly Leu Met Lys Asp Ala  
20 25 30

Phe Gln Pro His  
35 40 45

Gly Thr Val Asp Lys Lys Met Val Glu Lys Cys Trp Lys Leu Met Asp  
50 55 60

Lys Val Val Arg Leu Cys Gln Asn Pro Lys Leu Ala Leu Lys Asn Ser  
65 70 75 80

Pro Pro Tyr Ile Leu Asp Leu Leu Pro Asp Thr Tyr Gln His Leu Arg  
85 90 95

Thr Ile Leu Ser Arg Tyr Glu Gly Lys Met Glu Thr Leu Gly Glu Asn  
100 105 110

Glu Tyr Phe Arg Val Phe Met Glu Asn Leu Met Lys Lys Thr Lys Gln  
115 120 125

Thr Ile Ser Leu Phe Lys Glu Gly Lys Glu Arg Met Tyr Glu Glu Asn  
130 135 140

Ser Gln Pro Arg Arg Asn Leu Thr Lys Leu Ser Leu Ile Phe Ser His  
145 150 155 160

Met Leu Ala Glu Leu Lys Gly Ile Phe Pro Ser Gly Leu Phe Gln Gly  
165 170 175

Asp Thr Phe Arg Ile Thr Lys Ala Asp Ala Ala Glu Phe Trp Arg Lys  
180 185 190

Ala Phe Gly Glu Lys Thr Ile Val Pro Trp Lys Ser Phe Arg Gln Ala  
195 200 205

Leu His Glu Val His Pro Ile Ser Ser Gly Leu Glu Ala Met Ala Leu  
210 215 220

Lys Ser Thr Ile Asp Leu Thr Cys Asn Asp Tyr Ile Ser Val Phe Glu  
225 230 235 240

Phe Asp Ile Phe Thr Arg Leu Phe Gln Pro Trp Ser Ser Leu Leu Arg  
245 250 255

Asn Trp Asn Ser Leu Ala Val Thr His Pro Gly Tyr Met Ala Phe Leu  
260 265 270

Thr Tyr Asp Glu Val Lys Ala Arg Leu Gln Lys Phe Ile His Lys Pro  
275 280 285

Gly Ser Tyr Ile Phe Arg Leu Ser Cys Thr Arg Leu Gly Gln Trp Ala  
290 295 300

Ile Gly Tyr Val Thr Ala Asp Gly Asn Ile Leu Gln Thr Ile Pro His  
305 310 315 320

Asn Lys Pro Leu Phe Gln Ala Leu Ile Asp Gly Phe Arg Glu Gly Phe  
325 330 335

Tyr Leu Phe Pro Asp Gly Arg Asn Gln Asn Pro Asp Leu Thr Gly Leu  
340 345 350

Cys Glu Pro Thr Pro Gln Asp His Ile Lys Val Thr Gln Glu Gln Tyr  
355 360 365

Glu Leu Tyr Cys Glu Met Gly Ser Thr Phe Gln Leu Cys Lys Ile Cys  
370 375 380

Ala Glu Asn Asp Lys Asp Val Lys Ile Glu Pro Cys Gly His Leu Met  
385 390 395 400

Cys Thr Ser Cys Leu Thr Ser Trp Gln Glu Ser Glu Gly Gln Gly Cys  
405 410 415

Pro Phe Cys Arg Cys Glu Ile Lys Gly Thr Glu Pro Ile Val Val Asp  
420 425 430

Pro Phe Asp Pro Arg Gly Ser Gly Ser Leu Leu Arg Gln Gly Ala Glu  
435 440 445

Gly Ala Pro Ser Pro Asn Tyr Asp Asp Asp Asp Glu Arg Ala Asp  
450 455 460

Asp Thr Leu Phe Met Met Lys Glu Leu Ala Gly Ala Lys Val Glu Arg  
465 470 475 480

<211> 2721  
<212> DNA  
<213> Homo sapiens

<400> 263  
atggccggca acgtgaagaa gagctctggg gccggggcg gcacgggctc cgggggctcg 60  
ggttcggtg gcctgattgg gctcatgaag gacgccttcc agccgcacca ccaccaccac 120  
caccaccta gcccccaccc gccggggacg gtggacaaga agatggtgga gaagtgctgg 180  
aagctcatgg acaagggttgttgcgtt cagaacccaa agctggcgct aaagaatagc 240  
ccaccttata tcttagacct gctaccagat acctaccagc atctccgtac tatcttgtca 300  
agatatgagg ggaagatgga gacacttgga gaaaatgagt attttagggt gtttatggag 360  
aatttgatga agaaaactaa gcaaaccata agcctttca aggagggaaa agaaagaatg 420  
tatgaggaga attctcagcc taggcgaaac ctaaccaaac tgtccctcat cttagccac 480  
atgctggcag aactaaaagg aatctttcca agtggactct ttcagggaga cacatttcgg 540  
attactaaag cagatgctgc ggaattttgg agaaaagctt ttggggaaaa gacaatagtc 600  
ccttggaga gcttcgaca ggctctacat gaagtgcac ccacagttc tggctggag 660  
gccatggctc taaaatccac tattgatctg acctgcaatg attatatttc gtttttgaa 720  
tttgacatct ttacccgact cttagcccc tggcctctt tgctcaggaa ttggAACAGC 780  
cttgctgtaa ctcatcctgg ctacatggct ttttgacgt atgacgaagt gaaagctcg 840  
ctccagaaat tcattcacaa acctggcagt tatatcttcc ggctgagctg tactcgtctg 900  
ggtcagtggg ctattggta tgttactgct gatggaaaca ttctccagac aatccctcac 960  
aataaacctc tcttccaagc actgattgat ggcttcaggg aaggcttcta tttgttcct 1020  
gatggacgaa atcagaatcc tgatctgact ggcttatgtg aaccaactcc ccaagaccat 1080  
atcaaagtga cccaggaaca atatgaatta tactgtgaga tgggctccac attccaacta 1140  
tgtaaaatat gtgctgaaaa tgataaggat gtaaagattg agccctgtgg acacccatg 1200  
tgcacatcct gtcttacatc ctggcaggaa tcagaaggc agggctgtcc tttctgcccga 1260  
tgtgaaatta aaggtactga acccatcgtg gtagatccgt ttgatcctag agggagtggc 1320  
agcctgttga ggcaaggagc agagggagct ccctccccaa attatgatga tgatgatgat 1380  
gaacgagctg atgatactct cttcatgatg aaggaattgg ctggtgccaa ggtggAACGG 1440  
ccgccttctc cattctccat ggccccacaa gcttccttc ccccggtgcc accacgactt 1500  
gacccctgc cgcagcgagt atgtgttccc tcaagtgcctt ctgctttgg aactgcttct 1560

aaggctgctt ctggctccct tcataaagac aaaccattgc cagtacctcc cacacttcga 1620  
gatcttccac caccaccgcc tccagaccgg ccatattctg ttggagcaga atcccgacct 1680  
caaagacgcc ccttgccttg tacaccaggc gactgtccct ccagagacaa actgccccct 1740  
gtccctcta gccgccttgg agactcatgg ctgccccggc caatccccaa agtaccagta 1800  
tctgccccaa gttccagtga tccctggaca ggaagagaat taaccaacccg gcactcactt 1860  
ccattttcat tgccctcaca aatggagccc agaccagatg tgccctaggct cggaagcacg 1920  
ttcagtctgg atacctccat gagtatgaat agcagcccat tagtaggtcc agagtgtgac 1980  
caccccaaaa tcaaacccttc ctcatctgcc aatgccattt attctctggc tgccagacct 2040  
cttcctgtgc caaaaactgcc acctggggag caatgtgagg gtgaagagga cacagagtac 2100  
atgactccct cttccaggcc tctacggcct ttggatacat cccagagttc acgagcatgt 2160  
gattgcgacc agcagattga tagctgtacg tatgaagcaa tgtataatat tcagtcccag 2220  
gcccacatcta tcaccgagag cagcaccttt ggtgaagggg atttggccgc agcccatgcc 2280  
aacactggtc ccgaggagtc agaaaatgag gatgatgggt atgatgtccc aaagccacct 2340  
gtgccggccg tgctggcccg cogaactctc tcagatatct ctaatgccag ctccctctt 2400  
ggctgggtgt ctctggatgg tgatcctaca acaaatgtca ctgaaggttc ccaagttccc 2460  
gagaggcctc caaaaaccatt cccgcggaga atcaactctg aacggaaagc tggcagctgt 2520  
cagcaaggta gtggcctgc cgcctctgct gccaccgcct cacctcagct ctccagttag 2580  
atcgagaacc tcatgagtca ggggtactcc taccaggaca tccagaaagc tttggtcatt 2640  
gcccagaaca acatcgagat ggccaaaaac atcctccggg aatttggtttc catttcttct 2700  
cctgcccattg tagctaccta g 2721

<210> 264  
<211> 42  
<212> DNA  
<213> artificial

<220>  
<223> synthetic oligonucleotide probe for detecting mouse NPY mRNA

<400> 264  
gagggtcagt ccacacagcc ccattcgctt gttacctagc at 42

<210> 265  
<211> 45  
<212> DNA  
<213> artificial

<220>  
<223> synthetic oligonucleotide probe for detecting mouse cocaine- and amphetamine-regulated transcript mRNA

<400> 265  
tccttctcggt gggacgcata atccacggca gagtagatgt ccagg 45

<210> 266  
<211> 45  
<212> DNA  
<213> artificial

<220>  
<223> synthetic oligonucleotide probe for detecting mouse corticotropin-releasing hormone mRNA

<400> 266  
ccgataatct ccatcagttt cctgttgctg tgagcttgct gagct 45

<210> 267  
<211> 45  
<212> DNA  
<213> artificial

<220>  
<223> synthetic oligonucleotide probe for detecting mouse thyrotropin-releasing hormone mRNA

<400> 267  
aaccttactc ctccagaggt tccctgaccc aggcttccag ttgtg 45

<210> 268  
<211> 19  
<212> DNA  
<213> artificial

<220>  
<223> synthetic oligonucleotide for knocking down mouse Cbl expression

<400> 268  
gacactttcc ggattacta 19